

CLAIMS

1 1. A process for altering the host range of.
2 Bacillus toxins which comprises recombining in vitro
3 the variable region of two or more Bacillus toxin genes.

1 2. A process, according to claim 1, wherein the
2 Bacillus is a Bacillus thuringiensis.

1 3. A process, according to claim 2, wherein
2 variable regions of Bacillus thuringiensis var.
3 kurstaki HD-1 and Bacillus thuringiensis var.
4 kurstaki HD-73 are recombined in vitro to give genes
5 encoding chimeric toxins having altered host ranges.

1 4. DNA, denoted pEW3, encoding a chimeric toxin
2 having pesticidal activity, as follows:

3 (start HD-73) ATG GATAACAATC 400
4 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
5 GAAGTATTAG GTGGAGAAAG AATAGAACT GGTTACACCC CAATCGATAT 500
6 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
7 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
8 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT
9 AGAAGAATTC GCTAGGAACC AAGCCATTTC TAGATTAGAA GGAATAAGCA 700
10 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
11 ACTAATCCAG CATTAGAGAG AGAGATGCGT ATTCAATTCA ATGACATGAA 800
12 CAGTGGCCCTT ACAACCGCTA TTCTCTTTT TGCAGTTCAA AATTATCAAG
13 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
14 TTGAGAGATG TTTCAAGTGT TGGACAAAGG TGGGGATTG ATGCCGCGAC
15 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
16 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
17 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACT 1100
18 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
19 ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
20 GTATTAGAAA ATTTTGATGG TAGTTTTCGA GGCTCGGCTC AGGGCATAGA
TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA
ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCATT TTCCGCTATA 1400
TGGAAGTATG GGAAATGCAG TTCCACAACA ACCTATTGTT GCTCACTAG
GTCAGGGCGT GTATAGAACA CTTAGTCCA CTTTATATAG AAGACCTTTT 1500
AATATAGGGA TAAATAATCA ACAACTACT GTTCTTGACG GGACAGAATT
TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA

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21 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTCGTTC 1700
 22 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 (start HD-1) CCAACGT TTTCTTGGA GCATCGCAGT 1900
 23 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 24 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
 25 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTTCA
 26 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 27 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
 28 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200
 29 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
 30 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 31 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
 32 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 33 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAACAGAT GTGACGGATT
 34 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATTT 2500
 35 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 36 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600
 37 ATAGACAAC AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 38 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 39 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 40 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 41 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 42 TGTGCCAGGT ACGGGTTCCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900
 43 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 44 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000
 45 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 46 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 47 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 48 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 49 TGGAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 50 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 51 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 52 ATCTGCCCTGA GCTGTCTGTG ATTCGCGGTG TCAATGCGGC TATTTTTGAA 3400
 53 GAATTAGAAG GGCATTTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 54 TGTCAATAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGACGTGA 3500
 55 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT
 56 CTTCCGGAAT GGGAGCAGA AGTGTACAAA GAAGTTCGTG TCTGTCCGGG 3600
 57 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 58 GTTGCCTAAC CATTATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 59 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 60 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 61 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC
 62 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 63 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 64 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 65 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 66 GGAA (end HD-1)

and equivalent nucleotide sequences coding for toxin
EW3 with the following amino acid sequence:

MDNNPNINECIPYNCLSNPEVEVLGGGERIE
TGYTPIDISLSLTQFLLSEFVPGAGFVLGL
VDIIWGI FGPSQWDAFLVQIEQLINQRIEE
FARNQAISRLEGLSNLYQIYAESFREWEAD
PTNPALREEMRIQFNDMNSALTTAIFLFAV
QNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
RWGFDAATINSRYNDLTRLIGNYTDYAVRW
YNTGLERVWGPDSRDWVRYNQFRRELTLTV
LDIVALFFPNYDSRRYPVRTVSQLTREIYTN
FVLENFDGSGFRGSAQGGIERSIRSPHLM DIL
NSITITVTD AHRGYY YWSGHQIMASPVGFSG
PEFTFFPLYGTMGNAAPQQRIVAQLGGGVYR
TLESSTLYRRPFNIGINNQQLSVLDGTEFAY
GTSSSNLPSAVYRKSGTVDSDLDEIFPQNNNV
PPRGGFSSHRLSHVSMFRSGFSNSSVSIIIRA
PTFSWQHRS AEFNNIIFSSQITQIPLTKST
NLGSGTSSVVKGPBFTGGDILRRTSPGQIST
LRVNI TAPLSQRYRVRIRYASTTNLQFHTS
IDGRFINQGNFSSATMSSSGSNLQSGSFRTVG
FTTFFNFSSNGSSSVFTLSAHVFNSGNEVYID
RIEFVPAEVTFEAEYDLERAQKAVNELFTS
SNQIGLKTDTVTDYHIDQVSNLVECLSDFC
LDEKQELSEKVKHAKRLSDERNLLQDPNFR
GINRQLDRGWRGSTDITIQGGDDVFKENYV
TLLGT FDECYPTYLYQKIDESK LKAYTRYQ
LRGYIEDSQDLEIYLI RYN AKHETVNVPGT
GSLWFLSAQSPIGKCGEPNRCAPHLEWNPD
LDCSCRDGEEKCAHHSHHFSLDIDVGCTDLN
EDLG V W V I F K I K T Q D G H A R L G N L E F L E E K P
LVGEALARVKRAEKKWRDKREKLEWETNIV
YKEAKESVDALFVNSQYDQLQADTNIAMIH
AADKRVHSIREAYLP ELSVIFGVNA AIFEE
LEGRIFTA FSLYDARNVIKNGDFNNGLS CW
NVKGHV DVEEQNNQRSVLVLFEWEAEVSQE
VRVCPGRGYILRV TAYKEGYGEGCVTIHEI
ENNTDELKFSNCVEEEIYPNNTVTCNDYTV
NQEEYGGAYTSRNRGYNEAPSVPADYASVY
EEKSYTDGRRENPCFNRGYRDTYTPLPVGY
VTKELEYFPETDKVWIEIGETESTFIVDSV
ELLLMEE.

5. DNA, denoted pEW4, encoding a chimeric toxin,
having pesticidal activity, as follows:

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      (start HD-1)          ATGG ATAACAATCC GAACATCAAT
1  GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
2  TGGAGAAAGA ATAGAAACTG GTTACACCCC AATCGATATT TCCTTGTCGC
3  TAACGCAATT TCTTTTGAGT GAATTTGTTT CCGGTGCTGG ATTTGTGTTA 700
4  GGACTAGTTG ATATAATATG GGGGAATTTTT GGTCCCTCTC AATGGGACGC
5  ATTTCTGTGA CAAATTGAAC AGTTAATTAA CCAAAGAATA GAAGAATTCTG 800
6  CTAGGAACCA AGCCATTTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA
7  ATTTACGCAG AATCTTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900
8  ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA
9  CAACCGCTAT TCCTCTTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTTA 1000
10 TCAGTATATG TTCAAGCTGC AAATTTACAT TTATCAGTTT TGAGAGATGT
11 TTCAGTGTTC GGACAAAGGT GGGGATTTGA TGCCGCGACT ATCAATAGTC 1100
12 GTTATAATGA TTTAACTAGG CTTATTGGCA ACTATACAGA TTATGCTGTG
13 CGCTGGTACA ATACGGGATT AGAGCGTGTA TGGGGACCGG ATTCTAGAGA 1200
14 TTGGGTAAAG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG
15 ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTCGA 1300
16 ACAGTTTCCC AATTAACAAG AGAAATTTAT ACGAACCAG TATTAGAAAA
17 TTTTGATGGT AGTTTTCGTG GAATGGCTCA GAGAATAGAA CAGAATATTA 1400
18 GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCAT TTATACTGAT
19 GTGCATAGAG GCTTTAATTA TTGGTCAGGG CATCAAATAA CAGCTTCTCC 1500
20 TGTAGGGTTT TCAGGACCAG AATTCGCATT CCTTTTATTT GGGGATGCGG
21 GGAATGCAGC TCCACCCGTA CTTGTCTCAT TAACTGGTTT GGGGATTTTT 1600
22 AGAACATTAT CTTACCTTT ATATAGAAGA ATTATACTTG GTTCAGGCC
23 AAATAATCAG GAACTGTTTG TCCTTGATGG AACGGAGTTT TCTTTTGCCT 1700
24 CCCTAACGAC CAACTTGCCCT TCCACTATAT ATAGACAAAG GGGTACAGTC
25 GATTCAC TAG ATGTAAATACC GCCACAGGAT AATAGTGAC CACCTCGTGC 1800
26 GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
27 GAGCAGTTTA CACCTTGAGA GCTCAACGT (stop HD-1)
      (start HD-73)          CCT ATGTTCTCTT
28 GGATACATCG TAGTGCTGAA TTTAATAATA TAATTGCATC GGATAGTATT 1800
29 ACTCAAATCC CTGCAGTGAA GGGAACTTT CTTTTTAATG GTTCTGTAAT
30 TTCAGGACCA GGATTTACTG GTGGGACTT AGTTAGATTA AATAGTAGTG 1900
31 GAAATAACAT TCAGAAATAG GGGTATATTG AAGTTCCAAT TCACTTCCCA
32 TCGACATCTA CCAGATATCG AGTTCGTGTA CGGTATGCTT CTGTAACCCC 2000
33 GATTCACCTC AACGTTAATT GGGGTAATTC ATCCATTTTT TCCAATACAG
34 TACCAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTTGGT 2100
35 TATTTTGAAA GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG
36 TGTTAGAAAT TTTAGTGCGA CTGCAGGAGT GATAATAGAC AGATTTGAAT 2200
37 TTATTCCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG
38 CAGAAGGCGG TGAATGCGCT GTTTACGTCT ACAAACCAAC TAGGGCTAAA 2300
39 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT
40 ATTTATCGGA TGAATTTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
41 GTCAAACATG CGAAGCGACT CAGTGATGAA CGCAATTTAC TCCAAGATTC
42 AAATTTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCAGGAAGTA 2500
43 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAAGA AAATTACGTC
44 AACTATCAG GTACCTTTGA TGAGTGCTAT CCAACATATT TGTATCAAAA 2600
45 AATCGATGAA TCAAAATTAA AAGCCTTTAC CCGTTATCAA TTAAGAGGGT
46 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTCG CTACAATGCA 2700
47 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCCTTAT GGCCGCTTTC

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36 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGC GC GCCAC 2800
 37 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAG
 38 TGTGCCCATC ATTCGCATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900
 39 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC
 40 AAGATGGGCA CGCAAGACTA GGAATCTAG AGTTTCTCGA AGAGAAACCA 3000
 41 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG
 42 AGACAAACGT GAAAATTGG AATGGGAAAC AAATATCGTT TATAAGAGG 3100
 43 CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATCAATTA
 44 CAAGCGGATA CGAATATTGC CATGATTCAT GCGGCAGATA AACGTGTTCA 3200
 45 TAGCATTCTGA GAAGCTTATC TGCTGAGCT GTCTGTGATT CCGGGTGTCA
 46 ATGCGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTTCAC TGCATTCTCC 3300
 47 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTTTA ATAATGGCTT
 48 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400
 49 AACGTTGCGT CCTTGTGTTT CCGGAATGGG AAGCAGAAAG GTCACAAGAA
 50 GTTCGTGTCT GTCCGGGTCG TGGCTATATC CTTCGTGTCA CAGCGTACAA 3500
 51 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA
 CAGACGAACCT GAAGTTTAGC AACTGCGTAG AAGAGGAAAT CTATCCAAAT 3600
 AACACGGTAA CGTGAATGA TTATACTGTA AATCAAGAAG AATACGGAGG
 TGCGTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAG 3700
 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA
 GAGAATCCTT GTGAATTTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800
 AGTTGGTTAT GTGACAAAAG AATTAGAATA CTTCCAGAA ACCGATAAGG
 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTTATCGT GGACAGCGTG 3900
 GAATTACTCC TTATGGAGGA A (end HD-73)

52 and equivalent nucleotide sequences coding for toxin
 53 EW4 with the following amino acid sequence:

54 MDNNPNINECIPYNCLSNPEVEVEVLGGERIE
55 TGYTPIDISLSLTQFLLSEFVPGAGFVLGL
56 VDIIWGIFGPSQWDAFPVQIEQLINQRIEE
57 FARNQAI SRLEGLSNLYQIYAESFREWEAD
58 PTNFPALREEMRIQFNDMNSALTTAIPLLAV
59 QNYQVFLLSVYVQAANLHLSVLRDVSVFGQ
60 RWGFGAATINSRYNDLTRRLIGNYT DYAVRW
61 YNTGLERVWGFDSRDWVRYNQFRRELTTLTV
62 LDIVALF SNYDSRRYP IRTVSQLTREIYTN
63 PVL ENFDG SFRGM AQRIE QNIRQPHLM DIL
64 NSIT IYTDVHRGFNYWSGHQITASPVGFSG
65 PEF AFPLFGNAGNAAPPV LVSLTGLGIFRT
66 LSSPL YRRIILGSGPNNQELFVLDGTEFSF
67 ASLT TNLPSTIYRQRGTVD SLDVIFPQD NS
68 VPPRAGF SHRLSHVTMLSQAAGAVYTLRAQ
69 RPMFSWIHRSAEFNNIIASDSITQIPAVKG
70 NFLFN GSVISGPGFTGGDLVRLNSSSGNNIQ
71 NRGYIEVP IHF PSTSTRYRVRYASVTPI
72 HLN VNWGNSSIFSNTVPATATSLDNLQSSD
73 FGYFESANAF TSSLGNI VGV RNFSGTAGVI
74 IDRFEFIPVTATLEAEYNLERAQKAVNALF
75 TSTNQLGLKTNVTDYHIDQVSNLV TYLSDE
76 FCLDEKRELSEKVKHAKRLSDERNLLQDSN
77 FKDINRQPERSGWGGSTGITIQGGDDVFKEN
78 YVTL SGT FDECYFTYLYQK IDESKLKAFTR
79 YQLRGYIEDS QDLEIYLI RYN AKHETVNV P
80 GTGSLWPLSAQSPIGKCGEPNRCAPHLEWN
PDLDCSCRDG EKCAHHSHHFSLDIDV GCTD
LNE DLGVWVIFKIKTQDGHARLG NLEFLEE
KPLVGEALARVKRAEKKWRDKREKLEWETN
IVYKEAKESVDALFVNSQYDQLQADTNIAM
IHAADKRVHSIREAYLP ELSVIPGVNA AIF
EELEGRIFTAFSLYDARNVIKNGDFNNGLS
CWNVKGHV DVEEQNNQRSVLV VPEWEAEVS
QEV RVCPGRGYILRV TAYKEGYGEGCVTIH
EIE NNTDELKFSNCVEEEEIYPNNTVTCNDY
TVN QEEYGGAYTSRNRGYNEAPSVPADYAS
VYEEKSYTDGRRENPC EFNRGYRDTPLPV
GYVTKELEYFPETDKVWIEIGETEGTFIVD
SVELLLMEE.

1 6. DNA, denoted pACB-1, encoding a chimeric toxin,
2 having pesticidal activity, as follows:

3 (start HD-73) ATG GATAACAATC 400
 4 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 5 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTACACCC CAATCGATAT 500
 6 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
 7 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
 8 CAATGGGACG CATTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT
 9 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGACTAAGCA 700
 10 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
 11 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCATTCA ATGACATGAA 800
 12 CAGTGCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
 13 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
 14 TTGAGAGATG TTTCAAGTGT TGGACAAAGG TGGGGATTTG ATGCCGCGAC
 15 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
 16 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 17 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
 18 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
 19 ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
 20 GTATTAGAAA ATTTTGATGG TAGTTTTGGA GGCTCGGCTC AGGGCATAGA
 21 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 22 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA
 23 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCT TCCGCTATA 1400
 24 TGGAACTATG GGAATGCGG CTCCACAACA ACGTATTGTT GCTCAACTAG
 25 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 26 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 27 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 28 GAACGCTAGA TTCGCTGAAT GAAATACCGC CACAGAATAA CAACGTGCCA
 29 CCTAGGCAAG AATTTAGTCA TCGATTAGC CATGTTTCAA TGTTTCGTTT 1700
 30 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 31 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900
 32 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 33 AACAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
 34 GATTTACAGG AGGAGATATT CTTGGAAGAA CTTACCTGG CCAGATTTCA
 35 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 36 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
 37 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200
 38 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
 39 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 40 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
 41 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 42 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAACAGAT GTGACGGATT
 43 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTATTATC AGATGAATTT 2500
 44 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 45 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600
 46 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 47 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 48 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 49 TAAAGGCTTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 50 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 51 TGTGCCAGGT ACGGGTTCCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900
 52 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 53 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCC ATCATTGCGA 3000
 54 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC

55 TAGGTGATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 56 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 57 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 58 TGBAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 59 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 60 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 61 ATCTGCCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTTGAA 3400
 62 GAATTAGAAG GGCATTTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 63 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 64 AAGGGCATGT AGATGTAGAA GAACAAACA ACCAACGTTT GGTCTTGT
 65 CTTCCGGAAT GGGAGCAGA AGTGTCAACA GAAGTTCGTG TCTGTCCGGG 3600
 66 TCGTGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 67 GTTGCCTAAC CATTATGAG ATCGAGACA ATACAGACGA ACTGAAGTTT 3700
 68 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 69 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 70 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TCGTCAGTC
 71 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 72 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 73 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 74 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 75 GGAA (end HD-1)

76 and equivalent nucleotide sequences coding for toxin
 77 ACB-1 with the following amino acid sequence:

78 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
 79 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
 80 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
 81 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
 82 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
 83 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
 84 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 85 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
 86 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
 87 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
 88 N S I T I Y T D A H R G Y Y W S G H Q I M A S P V G F S G
 89 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
 90 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
 91 G T S S N L P S A V Y R K S G T V D S L N E I P P Q N N V
 92 P P R Q E F S H R L S H V S M F R S G F S N S S V S I I R A
 93 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
 94 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
 95 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
 96 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G

[illegible]

1 7. DNA, denoted pSYW1, encoding a chimeric toxin,
2 having pesticidal activity, as follows:

		(start	HD-73)	ATG	GATAACAATC	400
3						
4	CGAACATCAA	TGAATGCATT	CCTTATAATT	GTTTAAGTAA	CCCTGAAGTA	
5	GAAGTATTAG	GTGGAGAAAG	AATAGAACT	GGTTACACCC	CAATCGATAT	500
6	TTCTTTGTCT	CTAACGCAAT	TTCTTTTGAG	TGAATTTGTT	CCCGGTGCTG	
7	GATTTGTGTT	AGGACTAGTT	GATATAATAT	GGGGAATTTT	TGGTCCCTCT	600
8	CAATGGGACG	CATTTCTTGT	ACAAATTGAA	CAGTTAATTA	ACCAAAGAAT	
9	AGAAGAATTC	GCTAGGAACC	AAGCCATTTT	TAGATTAGAA	GGACTAAGCA	700
10	ATCTTTATCA	AATTTACGCA	GAATCTTTTA	GAGAGTGGGA	AGCAGATCCT	
11	ACTAATCCAG	CATTAAGAGA	AGAGATGCGT	ATTCAATTCA	ATGACATGAA	800
12	CAGTGGCCTT	ACAACCGCTA	TTCTCTTTT	TGCAGTTCAA	AATTATCAAG	
13	TTCTCTTTT	ATCAGTATAT	GTTCAAGCTG	CAAATTTACA	TTTATCAGTT	900
14	TTGAGAGATG	TTTCAGTGTT	TGGACAAAGG	TGGGGATTTG	ATGCCGCGAC	
15	TATCAATAGT	CGTTATAATG	ATTTAACTAG	GCTTATTGGC	AACTATACAG	1000
16	ATTATGCTGT	ACGCTGGTAC	AATACGGGAT	TAGAACGTGT	ATGGGGACCG	
17	GATTCTAGAG	ATTGGGTAAAG	GTATAATCAA	TTTAGAAGAG	AATTAACACT	1100
18	AACTGTATTA	GATATCGTTG	CTCTGTTCCC	GAATTATGAT	AGTAGAAGAT	
19	ATCCAATTTC	ACAGSTTTCC	CAATTAACAA	GAGAAATTTA	TACAAACCCA	1200
20	GTATTAGAAA	ATTTTGTATG	TAGTTTTTCA	GGCTCGGCTC	AGGGCATAGA	
21	AGGAAGTATT	AGGAGTCCAC	ATTTGATGGA	TATACTTAAC	AGTATAACCA	1300
22	TCTATACGGA	TGCTCATAAA	GGGGAATATT	ATTGGTCAGG	GCATCAAATA	
23	ATGGCTTCTC	CTGTAGGGTT	TTCGGGGCCA	GAATTCACTT	TTCCGCTATA	1400
24	TGGAAGTATG	GGAAATGCAG	CTCCACAACA	ACGTATTGTT	GCTCAACTAG	
25	GTCAGGGCGT	GTATAGAACA	TTATCGTCCA	CTTTATATAG	AAGACCTTTT	1500
26	AATATAGGGA	TAAATAATCA	ACAACATCT	GTTCTTGACG	GGACAGAATT	

27	TGCTTATGGA	ACCTCCTCAA	ATTTGCCATC	CGCTGTATAC	AGAAAAAGCG	1600
28	GAACGGTAGA	TTCGCTGGAT	GAAATACCGC	CACAGAATAA	CAACGTGCCA	
29	CCTAGGCAAG	GATTTAGTCA	TCGATTAAGC	CATGTTTCAA	TGTTTCGTTC	1700
30	AGGCTTTAGT	AATAGTAGTG	TAAGTATAAT	AAGAGCT (end hd-73)		
31	(start HD-1)	CCAACGT	TTTCTTGSCA	GCATCGCAST		1900
32	GCTGAATTTA	ATAATATAAT	TCCTTCATCA	CAAATTACAC	AAATACCTTT	
33	AACAAAATCT	ACTAATCTTG	GCTCTGGAAC	TTCTGTCTGT	AAAGSACCAG	2000
34	GATTTACAGG	AGGAGATATT	CTTCGAAGAA	CTTCACCTGG	CCAGATTTCA	
35	ACCTTAAGAG	TAAATATTAC	TGCACCATTA	TCACAAAGAT	ATCGGGTAAG	2100
36	AATTCGCTAC	GCTTCTACTA	CAAATTTACA	ATTCCATACA	TCAATTGACG	
37	GAAGACCTAT	TAATCAGGGT	AATTTTTCAG	CAACTATGAG	TAGTGGGAGT	2200
38	AATTTACAGT	CCGGAAGCTT	TAGGACTGTA	GGTTTTACTA	CTCCGTTTAA	
39	CTTTTCAAAT	GGATCAAGTG	TATTTACGTT	AAGTGCTCAT	GTCTTCAATT	2300
40	CAGGCAATGA	AGTTTATATA	GATCGAATTG	AATTTGTTCC	GGCAGAAAGTA	
41	ACCTTTGAGG	CAGAATATGA	TTTAGAAAGA	GCACAAAAGG	CGGTGAATGA	2400
42	GCTGTTTACT	TCTTCCAATC	AAATCGGGTT	AAAAACAGAT	GTGACGGATT	
43	ATCATATTGA	TCAAGTATCC	AATTTAGTTG	AGTGTTTATC	AGATGAATTT	2500
44	TGTCTGGATG	AAAAACAAGA	ATTGTCCGAG	AAAGTCAAAC	ATGCGAAGCG	
45	ACTTAGTGAT	GAGCGGAATT	TACTTCAAGA	TCCAAACTTC	AGAGGGATCA	2600
46	ATAGACAAC	AGACCGTGGC	TGGAGAGGAA	GTACGGATAT	TACCATCCAA	
47	GGAGGCGATG	ACGTATTCAA	AGAGAATTAC	GTTACGCTAT	TGGGTACCTT	2700
48	TGATGAGTGC	TATCCAACGT	ATTTATATCA	AAAAATAGAT	GAGTCGAAAT	
49	TAAAAGCCTA	TACCCGTTAT	CAATTAAGAG	GGTATATCGA	AGATAGTCAA	2800
50	GACTTAGAAA	TCTATTTAAT	TCGCTACAAT	GCAAAACATG	AAACAGTAAA	
51	TGTGCCAGGT	ACGGGTTCTT	TATGSCCGCT	TTCAGCCCCA	AGTCCAATCG	2900
52	GAAAGTGTTG	AGAGCCGAAT	CGATGCGGCG	CACACCTTGA	ATGGAAATCCT	
53	GACTTAGAAT	GTTCGTGTAG	GGATGGAGAA	AAGTGTGCCC	ATCATTCGCA	3000
54	TCATTTCTCC	TTAGACATTG	ATGTAGGATG	TACAGACTTA	AATGAGGACC	
55	TAGGTGTATG	GGTGATCTTT	AAGATTAAGA	CGCAAGATGG	GCACGCAAGA	3100
56	CTAGGSAATC	TAGAGTTTCT	CGAAGAGAAA	CCATTAGTAG	GAGAAGCGCT	
57	AGCTCGTGTG	AAAAGAGCGG	AGAAAAAATG	GAGAGACAAA	CGTGAAAAAT	3200
58	TGSAATGGGA	AACAAATATC	GTTTATAAAG	AGSCAAAAGA	ATCTGTAGAT	
59	GCTTTATTTG	TAAACTCTCA	ATATGATCAA	TTACAAGCGG	ATACGAATAT	3300
60	TGCCATGATT	CATGCGGCGAG	ATAAACGTGT	TCATAGCATT	CGAGAGGCTT	
61	ATCTGCCTGA	GCTGTCTGTG	ATTCCGGGTG	TCAATGCGGC	TATTTTGTGA	3400
62	GAATTAGAA	GGCGTATTTT	CACTGCATTC	TCCCTATATG	ATGCGAGAAA	
63	TGTCATTAAG	AATGGTGATT	TTAATAATGG	CTTATCCTGC	TGGAACGTGA	3500
64	AAGGGCATGT	AGATGTAGAA	GAACAAAACA	ACCAACGTTT	GGTCTTGTG	
65	CTTCCGGAAT	GGGAAGCAGA	AGTGTCACAA	GAAGTTCGTG	TCTGTCCGGG	3600
66	TCGTGGCTAT	ATCCTTCGTG	TCACAGCGTA	CAAGGAGGGA	TATGGAGAAG	
67	GTTGCGTAAC	CATTCATGAG	ATCGAGAAC	ATACAGACGA	ACTGAAGTTT	3700
68	AGCAACTGCG	TAGAAGAGGA	AATCTATCCA	AATAACACGG	TAACGTGTAA	
69	TGATTATACT	GTAATCAAG	AAGAATACGG	AGGTGCGTAC	ACTTCTCGTA	3800
70	ATCGAGGATA	TAACGAAGCT	CCTTCCGTAC	CAGCTGATTA	TGCGTCAGTC	
71	TATGAAGAAA	AATCGTATAC	AGATGGACGA	AGAGGAATC	CTTGTGAATT	3900
72	TAACAGAGGG	TATAGGGATT	ACACGCCACT	ACCAGTTGGT	TATGTGACAA	
73	AAGAATTAGA	ATACTTCCCA	GAAACCGATA	AGGTATGGAT	TGAGATTGGA	4000
74	GAAACGGAAG	GAACATTTAT	CGTGGACAGC	GTGGAATTAC	TCCTTATGGA	
75	GGAA (end HD-1)					

76 and equivalent nucleotide sequences coding for toxin
 77 SYW1 with the following amino acid sequence:

78 MDNNPNINECIPYNCLSNPEVEEVLGGGERIE
 79 TGYTFIDISLSLTQFLLSSEFVPGAGFVVLGL
 80 VDI IWGIFGPSQWDAFLVQIEQLINQRIEE
 81 FARNQAISRLEGLSNLYQIYAESFREWEAD
 82 PTNPALREEMRIQFNDMNSALTTAIPLFAV
 83 QNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
 84 RWGFDAAATINSRYNDLTRLIGNYTDYAVRW
 85 YNTGLERVWGPDSRDWVRYNQFRRELTLTV
 86 LDIVALFPNYDSRRYPPIRTVSQLTREIYTN
 87 PVLENFDGSGFRGSAQGI EGSI RSPHLM DIL
 88 NSIT IYTD AHKG EY YWSGH QIMASPVGFGSG
 89 PEFTTFPLYGT MGN A A PQQRI VAQLGQGVYR
 90 TLSSTLYRRPFNIGINNQQLSVLDGTEFAY
 91 GTSSSNLPSAVYRKSGTVDSLDEIPPQNNNV
 92 PPRQGFSHRLSHVSMFRSGFSSSVSIIIRA
 93 PTFSSWQHRS AEFNNIIPSSQITQIPLTKST
 94 NLGSGT SVVKGP GFTGGDILRRTSPGQIST
 95 LRVNITAPLSQR YRVRI RYASTTNLQFHTS
 96 IDGRPINQGNFSSATMSSSGSNLQSGSFRTVG
 97 FTTPFNFSNGSSVFTLSAHVFNSGNEVYID
 98 RIEFVPAEVTFEAEYDLERAQKAVNELFTS
 99 SNQIGLKT DVT D YHIDQVSNLVECLSD EFC
 100 LDEKQELSEKVKHAKRLSDERNLLQDPNFR
 101 GINRQLDRGWRGSTDITIQQGGDDVFKENYV
 102 TLLGTFDECYPTYLYQKIDESK LKAYTRYQ
 103 LRGYIEDSQDLEIYLI RYN AKHETVNVPGT
 104 GSLWPLSAQSPIGKCGEPNRCAPHLEWNPD
 105 LDCSCRDGEKCAHHSHHFSLDIDVGCTDLN
 106 EDLG V W V I F K I K T Q D G H A R L G N L E F L E E K P
 107 LVGEALARVKRAEK KWRDKREKLEWETNIV
 108 YKEAKESVDALFVNSQYDQLQADTNIAMIH
 109 AADKRVHSIREAYLPELSVIPGVNA AIFEE
 110 LEGRIFTAFSLYDARNVIKNGDFNNGLS CW
 111 NVKGHV DVEEQNNQRSVLVLPEWEAEVSQE
 112 VRVCPGRGYILRV TAYKEGYGEGCVTIHEI
 113 ENNTDELKFSNCVEEEIYPNNTVTCNDYTV
 114 NQEEYGGAYT SRNRGYNEAPSVPADYASVY
 115 EEKSYTDGRRENPCFNRGYR DYTPLPVGY
 116 VTKELEYFPETDKVWIEIGETEGTFIVDSV
 117 ELLLMEE.

1 8. A chimeric toxin, EW3, having pesticidal
2 activity, having the following amino acid sequence:

3 MDNNPNIN ECIPYNCLSNPEVEVLGGERIE
4 TGYTPIDISLSLTQFLLSEFVPGAGFVLGL
5 VDIIWGIFGFSQWDAFLVQIEQLINQRIEE
6 FARNQAI SRLEGLSNLYQIYAESFREWEAD
7 PTNPALREEMRIQFNDMNSALTTAIFLFAV
8 QNYQVPLLSVYVQAANLHLSVL RDVSVFGQ
9 RWGFDAATINSRYNDLTRLIGNYT DYAVRW
10 YNTGLERVWGPDSRDWVRYNQFRRELT LT V
11 LDIVALFPNYDSRRYP IRTVSQLTREIYTN
12 PVLENFDGSGFRGSAQGIERSIRSPHLM DIL
13 NSITIIYTD AHRGYYYWSGHQIMASPVGFSG
14 PEFTTFPLYGTMGNAAPQQR1VAQLGQGVYR
15 TLSSTLYRRPFNIGINNQQLSVL DGT EFAY
16 GTSSNLPSAVYRKSGTVDSLDEIPPQNNNV
17 PPRQGFSHRLSHVSMFRSGFSNSSVSIIRA
18 PTFSWQHRSAEFNNIIPSSQITQIFLTKST
19 NLGSGT SVVKGP GFTGGDILRRTSPGQIST
20 LRVNITAPLSQRYRVRIRYASTTNLQFHTS
21 IDGRFINQGNFSATMSSSGSNLQSGSFRTVG
22 FTTPFNF SNGSSVFTLSAHVFNSGNEVYID
23 RIEFVPAEVTFEAEYDLERAQKAVNELFTS
24 SNQIGLKT DVTDYHIDQVSNLVECLSD EFC
25 LDEKQELSEKVKHAKRLSDERNLLQDPNFR
26 GINRQLDRGW RGSTDITIQGGDDVFKENYV
27 TLLGT FDECYPTYLYQKIDESK LKAYTRYQ
28 LRGYIEDSQDLEIYLIRYN AKHETVNVPGT
29 GSLWPLSAQSPIGKCGEPNRCAPHLEWNP D
30 LDCSCR DGEKCAHHSHHFSLDIDVGC TDLN
31 EDLGVWVIFKIKTQDGHAPLG NLEFLEEK P
32 LVGEALARVKRAEKKWRDKREKLEWETNIV
33 YKEAFESVDALFVNSQYDQLQADTNIAMIH
34 AADKR VH SIREAYLP ELSV1PGVNAAIFEE
35 LEGRIFTAFSLYDARNV IKNBDFNNGLS CW
36 NVKGHV DVEEONNQRSVLVLPEWEAEV SQE
37 VRVCPGRGYILRV TAYKEGYGEGCVTIHEI
38 ENNTDELKFSNCVEEEIYPNNTVTCNDYTV
39 NQEEYGGAYTSRN RGYNEAPSVPADYASVY
40 EEKSYTDGRRENPC EFNRGYRDYTF LPVGY
41 VTKELEYFPETDKVWIEIGETEGT FIVDSV
42 ELLLMEE

43 and muteins thereof which do not alter the protein
44 secondary structure.

1 9. A chimeric toxin, EW4, having pesticidal
2 activity, having the following amino acid sequence:

3 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
5 V D I I W G I F G P S Q W D A F P V Q I E Q L I N Q R I E E
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L L A V
8 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
11 L D I V A L F S N Y D S R R Y P I R T V S Q L T R E I Y T N
12 P V L E N F D G S F R G M A Q R I E Q N I R Q P H L M D I L
13 N S I T I Y T D V H R G F N Y W S G H Q I T A S P V G F S G
14 P E F A F P L F G N A G N A A P P V L V S L T G L G I F R T
15 L S S P L Y R R I I L G S G P N N Q E L F V L D G T E F S F
16 A S L T T N L P S T I Y R Q R G T V D S L D V I P P Q D N S
17 V P P R A G F S H R L S H V T M L S Q A A G A V Y T L R A Q
18 R P M F S W I H R S A E F N N I I A S D S I T Q I P A V K G
18 N F L F N G S V I S G P G F T G G D L V R L N S S G N N I Q
20 N R G Y I E V P I H F P S T S T R Y R V R V R Y A S V T P I
21 H L N V N W G N S S I F S N T V P A T A T S L D N L Q S S D
22 F G Y F E S A N A F T S S L G N I V G V R N F S G T A G V I
23 I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F
24 T S T N Q L G L K T N V T D Y H I D Q V S N L V T Y L S D E
25 F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N
26 F K D I N R Q P E R G W G G S T G I T I Q G G D D V F K E N
27 Y V T L S G T F D E C Y P T Y L Y Q K I D E S K L K A F T R
28 Y Q L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P
29 G T G S L W P L S A Q S P I G K C G E P N R C A P H L E W N
30 P D L D C S C R D G E K C A H H S H H F S L D I D V G C T D
31 L N E D L G V W V I F K I K T Q D G H A R L G N L E F L E E
32 K P L V G E A L A R V K R A E K K W R D K R E K L E W E T N
33 I V Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M
34 I H A A D K R V H S I R E A Y L P E L S V I P G V N A A I F
35 E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S
36 C W N V K G H V D V E E Q N N Q R S V L V V P E W E A E V S
37 Q E V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H
38 E I E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y
39 T V N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S
40 V Y E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V
41 G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D
42 S V E L L L M E E

43 and muteins thereof which do not alter the protein
44 secondary structure.

-58-

1 10. A chimeric toxin, ACB-1, having pesticidal
2 activity, having the following amino acid sequence:

3 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
5 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
8 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
11 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
12 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
13 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G
14 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
16 G T S S N L P S A V Y R K S G T V D S L N E I P P Q N N V
17 P P R Q E F S H R L S H V S M F R S G F S N S S V S I I R A
18 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
19 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
20 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
21 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
23 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
24 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
26 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
27 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
28 G S L W P L S A Q S P I G K C G E F N R C A P H L E W N P D
30 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
31 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K F
32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
33 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
36 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
37 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
39 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
42 E L L L M E E

43 and muteins thereof which do not alter the protein
44 secondary structure.

1 11. A chimeric toxin, SYW1, having pesticidal
2 activity, having the following amino acid sequence:

3 MDNNPNIN ECIPYNCLSNPEVEVELGGERIE
4 TGYTFIDISLSLTQFLLSEFVPGAGFVLGL
5 VDIIWGIFGPSQWDAFLVQIEQLINQRIEE
6 FARNQAISRLEGLSNLYQIYAESFREWEADV
7 PTNPALREEMRIQFNDMMNSALTTAIPLFAV
8 QNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
9 RWGFDAATINSRYNDLTRLIGNYT DYAVRW
10 YNTGLERVWGPDSRDWVRYNQFRRELTLTV
11 LDIVALFPNYDSRRYP IRTVSQLTREIYTN
12 PVLENFDGGSFRGSAQGGIEGSI RSPHLMGDI
13 NSITIIYTDAHKGEY YWSGHQIMASPVGFSG
14 PEFTTFPLYGTMGNAAPQQQRIVAQLGGVYR
15 TSSSTLYRRPFFNIGINNQQLSVLDGTEFAY
16 GTSSSNLP S AVYRKSGTVDSGFSNS SVSIRA
17 PPRQGFSHRLSHVSMF RSGFSNS SVSIRA
18 PTFSSWQHRS AEFNNIIPSSSQITQIPLTKST
19 NLGSGTSSVVKGP GFTGGDILRRTSPGQIST
20 LRVNRITAPLSQR YRVRIRYASTTNLQFHTS
21 IDGRPINQGNFSATMS SSGSNLQSGSFRTVG
22 FTTPFNF SNGSSSVFTLSAHVFNSGNEVYID
23 RIEFVPAEVTFEAEYDLER AQKAVNELFTS
24 SNQIGLKT DVTDYHIDQVSNLVECLSD EFC
25 LDEKQELSEKVKHAKRLSDERNLLQDPNFR
26 GINRQLDRGW RGSTDTITIQGGDDVFKENYV
27 TLLGTFDECYPT YLYQKIDESK LKAYTRYQ
28 LRGYIEDSQDLEIYLIRYN AKHETVNVPGT
29 GSLWFLSAQSP I GKC GEPNRCAPHLEWNP D
30 LDCSCR DGEKCAHHS HFSLDIDV GCTDLN
31 EDLG V W V I F K I K T Q D G H A R L G N L E F L E E K P
32 LVGEALARVKRAEKKWRD KREKLEWETNIV
33 YKEAKESVDALFVNSQYDQLQADTNIAMIH
34 AADKRVHSIREAYLP ELSVIPGVNA AIFEE
35 LEGRIFTAFSLYDARNV IKN GDFNNGLS CW
36 NVKGHV DVEEQNNQR SVLVLP EWAEV SQE
37 VRVCPGRGYILRV TAYKEGGY GEGCVTIHEI
38 ENNTDELKFSNCVEEEIYPNNTVTCNDYTV
39 NQEEYGGAYTSRNRGYNEAPSVPADYASVY
40 EEKSYTDGRRENPC EFN RGYRDTPLPVG Y
41 VTKELEYFPETDKVWIEIGETEGTFIVDSV
42 ELLMEE

43 and muteins thereof which do not alter the protein
44 secondary structure.

1 12: A pesticidal composition comprising pesti-
2 cide-containing substantially intact cells having
3 prolonged pesticidal activity when applied to the
4 environment of a target pest, wherein said pesticide,
5 is a chimeric toxin, is intracellular and is produced
6 as a result of expression of a heterologous gene
7 encoding said chimeric toxin in said cell.

1 13. A pesticidal composition according to claim 12,
2 wherein said cells are killed under protease deacti-
3 vating or cell wall strengthening conditions, while
4 retaining pesticidal activity.

1 14. A pesticidal composition, according to claim 12,
2 wherein said cells are prokaryotes selected from the
3 group consisting of Enterobacteriaceae, Bacillaceae,
4 Rhizobiaceae, Spirillaceae, Lactobacillaceae, Pseudo-
5 monadaceae, Azotobacteraceae, and Nitrobacteraceae; or
6 lower eukaryotes selected from the group consisting
7 of Phycomycetes, Ascomycetes, and Basidiomycetes.

1 15. A pesticidal composition, according to claim 14,
2 wherein said prokaryote is a Bacillus specie selected
3 from a pesticide-producing strain of Bacillus thurin-
4 giensis, consisting of B. thuringiensis M-7, B. thurin-
5 giensis var. kurstaki, B. thuringiensis var. finitimus,
6 B. thuringiensis var. alesti, B. thuringiensis var.
7 sotto, B. thuringiensis var. dendrolimus, B. thurin-
8 giensis var. kenyae, B. thuringiensis var. galleriae,
9 B. thuringiensis var. canadensis, B. thuringiensis var.
10 entomocidus, B. thuringiensis var. subtoxicus, B.
11 thuringiensis var. aizawai, B. thuringiensis var. morri-
12 soni, B. thuringiensis var. ostrinae, B. thuringiensis
13 var. tolworthi, B. thuringiensis var. darmstadiensis,

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14 B. thuringiensis var. toumanoffi, B. thuringiensis var.
15 kyushuensis, B. thuringiensis var. thompsoni, B.
16 thuringiensis var. pakistani, B. thuringiensis var.
17 israelensis, B. thuringiensis var. indiana, B. thurin-
18 giensis var. dakota, B. thuringiensis var. tohokuensis,
19 B. thuringiensis var. kumanotoensis, B. thuringiensis
20 var. tochigiensis, B. thuringiensis var. colmeri,
21 B. thuringiensis var. wuhanensis, B. thuringiensis
22 var. tenebrionis, B. thuringiensis var. thuringiensis,
23 and other Bacillus species selected from B. cereus, B.
24 moritai, B. popilliae, B. lentimorbus, and B. sphaericus.

1 16. A method of protecting plants against pests
2 which comprises applying to said plants an effective
3 amount of a pesticidal composition comprising pesti-
4 cide-containing substantially intact unicellular
5 microorganisms, wherein said pesticide is a chimeric
6 toxin, is intracellular, and is produced as a result
7 of expression of a heterologous gene encoding said
8 chimeric toxin in said microorganism, and said micro-
9 organism is treated under conditions which prolong
10 the pesticidal activity when said composition is applied
11 to the environment of a target pest.

1 17. A method according to claim 16, wherein said
2 microorganisms are prokaryotes selected from the
3 group consisting of Enterobacteriaceae, Bacillaceae,
4 Rhizobiaceae, Spirillaceae, Lactobacillaceae, Pseudo-
5 monadaceae, Azotobacteraceae, and Nitrobacteraceae; or
6 lower eukaryotes, selected from the group consisting
7 of Phycomycetes, Ascomycetes, and Basidiomycetes.

1 18. A method according to claim 16, wherein said
2 unicellular microorganisms are killed under protease
3 deactivating or cell wall strengthening conditions,
4 while retaining pesticidal activity.

1 19. Substantially intact unicellular microorganism
2 cells containing an intracellular chimeric toxin, which
3 toxin is a result of expression of a heterologous
4 gene encoding said chimeric toxin, wherein said cells
5 are killed under protease deactivating or cell wall
6 strengthening conditions, while retaining pesticidal
7 activity when said cell is applied to the environment
8 of a target pest.

1 20. Cells according to claim 19, wherein said
2 microorganism is a Pseudomonad and said toxin is
3 derived from a B. thuringiensis.

1 21. A pesticidal composition, according to claim
2 12, wherein said gene, denoted pEW3, encoding a
3 chimeric toxin, is as follows:

4 (start HD-73) ATG GATAACAATC 400
5 CGAACATCAA TGAATGCATT CTTATAATT GTTTAAGTAA CCCTGAAGTA
6 GAAGTATTAG GTGGAGAAAG AATAGAACT GGTACACCC CAATCGATAT 500
7 TTCCTTGCTG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
8 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
9 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT
10 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGAATAAGCA 700
11 ATCTTTATCA AATTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
12 ACTAATCCAG CATTAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
13 CAGTGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
14 TTCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
15 TTGAGAGATG TTTCAGTGT TGGACAAAGG TGGGGATTTG ATGCCGCGAC
TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACT 1100
AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
GTATTAGAAA ATTTTGATGG TAGTTTTCSA GGCTCGGCTC AGGGCATAGA

16 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 17 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA
 18 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCT TTCCGCTATA 1400
 19 TGGAACTATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
 20 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 21 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 22 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 23 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
 24 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTTCGTTT 1700
 25 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 26 (start HD-1) CCAACGT TTTCTTGSCA GCATCGCAGT 1900
 27 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 28 AACAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTGCTT AAAGGACCAG 2000
 29 GATTTACAGG AGGAGATATT CTTGGAAGAA CTTACCTGG CCAGATTTCA
 30 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 31 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
 32 GAAGACCTAT TAATCAGGGT AATTTTTTCA CAACTATGAG TAGTGGGAGT 2200
 33 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
 34 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 35 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
 36 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 37 GCTGTTTACT TCTTCCAATC AAATCGGGT AAAACAGAT GTGACGGATT
 38 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTTATC AGATGAATTT 2500
 39 TGTCTGGATG AAAAACAAAG ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 40 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600
 41 ATAGACAAC AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 42 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 43 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAT
 44 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 45 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 46 TGTGCCAGGT ACGGGTTTCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900
 47 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 48 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCC ATCATTGCGA 3000
 49 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 50 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 51 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAAGCGCT
 52 AGCTCGTGTG AAAAGAGCGG AGAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 53 TGGAAATGGG AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 54 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 55 TGCCATGATT CATGCGGCG AGAACGTTG TCATAGCATT CGAGAAGCTT
 56 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGA 3400
 57 GAATTAGAAG GGCATATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 58 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 59 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT
 60 CTTCGGAAT GGGAAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600
 61 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 62 GTTGCCTAAC CATTCATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 63 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 64 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 65 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TCGTCAAGT
 66 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 67 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 68 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 69 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAAATTAC TCCTTATGGA
 70 GGAA (end HD-1)

52 and equivalent nucleotide sequences coding for toxin
53 EW3 with the following amino acid sequence:

54 MDNNPNININECIPYNCCLSNPEVEVEVLGGGERIE
55 TGYTPIDISLSLTQFLLSSEFVPGAGFVLGL
56 VDIIWGIFGPSQWDAFLVQIEQLINQRIEE
57 FARNQAI SRLEGLSNLYQIYAESFREWEAD
58 PTNPALREEMRIQFNDMNSALTTAIPLFAV
59 QNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
60 RWGFDAAATINSRYNDLTRLIGNYTDYAVRW
61 YNTGLERVWGPDSRDWVRYNQFRRELTLTV
62 LDIVALFFPNYDSRRYPPIRTVSQLTREIYTN
63 PVLENFDGGSFRGSAQGIERSIRSPHLM DIL
64 NSITIIYTD AHRGYYYWSGHQIMASPVGFSG
65 PEFTTFPLYGTMGNAAPQQRIVAQLGGGVYR
66 TSSSTLYRRPFNIGINNQQLSVLDGTEFAY
67 GTSSNLP S AVYRKSGTVDSLDEIPPNNNV
68 PPRQGF SHRLSHVSMFRSGFSNSSVSIIRA
69 PTFSWQHRS AEFNNIIPSSQITQIPLTKST
70 NLGSGT SVVKGPFGFTGGDILRRTSPGQIST
71 LRVNITAPLSQR YRVRIRYASTTNLQFHTS
72 IDGRPINQGNFSATMSSSGSNLQSGSFRTVG
73 FTTFFNF SNGSSVFTLSAHVFNSGNEVYID
74 RIEFVPAEVTFEAEYDLERAQKAVNELFTS
75 SNQIGLKT DVTDYHIDQVSNLVECLSD EFC
76 LDEKQELSEKVKHAKRLSDERNLLQDPNFR
77 GINRQLDRGWRGSTDITIQQGGDDVFKENYV
78 TLLGTFDECYPTYLYQKIDESK LKAYTRYQ
79 LRGYIEDS QDLEIYLIRYN AKHETVNVPGT
80 GSLWPLSAQSPIGKCGEPNRCAPHLEWNP D
71 LDCSCR DGEKCAHHSHHFSLDIDVGCTDLN
72 EDLGVWVIFKIKTQDGHARLGNLEFLEEK P
73 LVGEALARVKRAEKKWRDKREKLEWETNIV
74 YKEAKESVDALFVNSQYDQLQADTNIAMIH
75 AADKRVHSIREAYLPELSVIFGVNA AIFEE
76 LEGRIFTAFSLYDARNV IKN GDFNNGLS CW
77 NVKGHV DVEEQNNQRSVLVLPEWEAEVSOE
78 VRVCPGRGYILRV TAYKEGYGEGCVTIHEI
79 ENNTDELKFSNCVEEEIYPNNTVTCNDYTV
80 NQEEYGGAYTSRNRGYNEAPSVPADYASVY
81 EEKSYTDGRRENPCFENRGYRDYTPLPVGY
82 VTKELEYFPETDKVWIEIGETEGTFIVDSV
83 ELLLMEE.

1 22. A pesticidal composition, according to claim
2 12, wherein said gene, denoted pEW4, encoding a
3 chimeric toxin, is as follows:

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4           (start HD-1)                   ATGG ATAACAATCC GAACATCAAT
5           GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
6           TGGAGAAAGA ATAGAAACTG GTTACACCCC AATCGATATT TCCTTGTCGC
7           TAACGCAATT TCTTTTGAGT GAATTTGTTC CCGGTGCTGG ATTTGTGTTA 700
8           GGACTAGTTG ATATAATATG GGGAAATTTT GGTCCCTCTC AATGGGACGC
9           ATTTCTGTGA CAAATTGAAC AGTTAATTAA CCAAAGAATA GAAGAATTCTG 800
10           CTAGGAACCA AGCCATTTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA
11           ATTTACGCAG AATCTTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900
12           ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA
13           CAACCGCTAT TCCTCTTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTTA 1000
14           TCAGTATATG TTCAAGCTGC AAATTTACAT TTATCAGTTT TGAGAGATGT
15           TTCAGTGTTC GGACAAAGGT GGGGATTTGA TGCCGCGACT ATCAATAGTC 1100
16           GTTATAATGA TTTAACTAGG CTTATTGGCA ACTATACAGA TTATGCTGTG
17           CGCTGGTACA ATACGGGATT AGAGCGTGTA TGGGGACCGG ATTCTAGAGA 1200
18           TTGGGTAAAG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG
19           ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTCGA 1300
20           ACAGTTTCCC AATTAACAAG AGAAATTTAT ACGAACCCAG TATTAGAAAA
21           TTTTGATGGT AGTTTTCGTG GAATGGCTCA GAGAATAGAA CAGAATATTA 1400
22           GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCAT TTATACTGAT
23           GTGCATAGAG GCTTTAATTA TTGGTCAGGG CATCAAATAA CAGCTTCTCC 1500
24           TGTAGGGTTT TCAGGACCAG AATTCGCATT CCCTTTATTT GGGGAATGCGG
25           GGAATGCAGC TCCACCCGTA TTGTCTCAT TAAGTGGTTT GGGGATTTTT 1600
26           AGAACATTAT CTTACCTTTT ATATAGAAGA ATTATACTTG GTTCAGGCCC
27           AAATAATCAG GAACTGTTTG TCCTTGATGG AACGGAGTTT TCTTTTGCCCT 1700
28           CCCTAACGAC CAACTGCGCT TCCACTATAT ATAGACAAAG GGGTACAGTC
29           GATTCAGTAG ATGTAATACC GCCACAGGAT AATAGTGTAC CACCTCGTGC 1800
30           GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
31           GAGCAGTTTA CACCTTGAGA GCTCAACGT (stop HD-1)
32           (start HD-73)                   CCT ATGTTCTCTT
33           GGATACATCG TAGTGCTGAA TTTAATAATA TAATTGCATC GGATAGTATT 1800
34           ACTCAAATCC CTGCAGTGAA GGGAAACTTT CTTTTTAATG GTTCTGTAAT
35           TTCAGGACCA GGATTTACTG GTGGGGACTT AGTTAGATTA AATAGTAGTG 1900
36           GAAATAACAT TCAGAATAGA GGGTATATTG AAGTTCCAAT TCACTTCCCA
37           TCGACATCTA CCAGATATCG AGTTCGTGTA CGGTATGCTT CTGTAACCCC 2000
38           GATTCACCTC AACGTTAATT GGGGTAATTC ATCCATTTTT TCCAATACAG
39           TACCAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTTGGT 2100
40           TATTTTGAAA GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG
41           TGTTAGAAAT TTTAGTGGGA CTGCAGGAGT GATAATAGAC AGATTTGAAT 2200
42           TTATTCCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG

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30 CAGAAGGCGG TGAATGCGCT GTTTACGTCT ACAAACCAAC TAGGGCTAAA 2300
 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT
 31 ATTTATCGGA TGAATTTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
 GTCAAACATG CGAAGCGACT CAGTGATGAA CGCAATTTAC TCCAAGATTC
 32 AAATTTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCGBAAGTA 2500
 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAAGA AAATTACGTC
 33 ACCTATCAG GTACCTTTGA TGAGTGCTAT CCAACATATT TGTATCAAAA 2600
 AATCGATGAA TCAAAATTAA AAGCCTTTAC CCGTTATCAA TTAAGAGGGT
 34 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTCG CTACAATGCA 2700
 35 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCTTAT GGCCGCTTTC
 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCBCGCCAC 2800
 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAG
 36 TGTGCCCATC ATTCGCATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900
 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC
 37 AAGATGGSCA CGCAAGACTA GGGAACTAG AGTTTCTCGA AGAGAAACCA 3000
 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG
 38 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAAGAGG 3100
 CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATCAATTA
 39 CAAGCGGATA CGAATATTGC CATGATTCAT GCGGCAGATA AACGTGTTCA 3200
 TAGCATTCGA GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA
 40 ATGCGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTTCAC TGCATTCTCC 3300
 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTTTA ATAATGGCTT
 41 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAACAACC 3400
 AACGTTGCGT CCTTGTGTT CCGGAATGGG AAGCAGAAAT GTCACAAGAA
 42 GTTCGTGTCT GTCCGGGTCG TGGCTATATC CTTCTGTCA CAGCGTACAA 3500
 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA
 43 CAGACGAAC GAAGTTTAGC AACTGCGTAG AAGAGGAAAT CTATCCAAT 3600
 AACACGGTAA CGTGTAAATG TTATACTGTA AATCAAGAAG AATACGGAGG
 44 TGCCTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAG 3700
 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA
 45 GAGAATCCTT GTGAATTTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800
 AGTTGGTTAT GTGACAAAAG AATTAGAATA CTTCCAGAA ACCGATAAGG
 46 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTTATCGT GGACAGCGTG 3900
 51 GAATTACTCC TTATGGAGGA A (end HD-73)

52 and equivalent nucleotide sequences coding for toxin
 53 EW4 with the following amino acid sequence:

54 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
 T G Y T P I D I S L S L T Q F L L S E F V F G A G F V L G L
 55 V D I I W G I F G P S Q W D A F P V Q I E Q L I N Q R I E E
 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
 56 P T N P A L R E E M R I Q F N D M N S A L T T A I P L L A V
 Q N Y Q V F L L S V Y V Q A A N L H L S V L R D V S V F G Q
 57 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
 58 L D I V A L F S N Y D S R R Y P I R T V S Q L T R E I Y T N
 P V L E N F D G S F R G M A Q R I E Q N I R Q P H L M D I L
 59 N S I T I Y T D V H R G F N Y W S G H Q I T A S P V G F S G
 60 P E F A F P L F G N A G N A A P P V L V S L T G L G I F R T
 61

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62 L S S P L Y R R I I L G S G P N N Q E L F V L D G T E F S F
 63 A S L T T N L P S T I Y R Q R G T V D S L D V I P P Q D N S
 64 V P P R A G F S H R L S H V T M L S Q A A G A V Y T L R A Q
 65 R P M F S W I H R S A E F N N I I A S D S I T Q I P A V K G
 66 N F L F N G S V I S G P G F T G G D L V R L N S S G N N I Q
 67 N R G Y I E V P I H F P S T S T R Y R V R V R Y A S V T P I
 68 H L N V N W G N S S I F S N T V P A T A T S L D N L Q S S D
 69 F G Y F E S A N A F T S S L G N I V G V R N F S G T A G V I
 70 I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F
 71 T S T N Q L G L K T N V T D Y H I D Q V S N L V T Y L S D E
 72 F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N
 73 F K D I N R Q P E R G W G G S T G I T I Q G G D D V F K E N
 74 Y V T L S G T F D E C Y F T Y L Y Q K I D E S K L K A F T R
 75 Y Q L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P
 76 G T G S L W P L S A Q S P I G K C G E P N R C A P H L E W N
 77 P D L D C S C R D G E K C A H H S H H F S L D I D V G C T D
 78 L N E D L G V W V I F K I K T Q D G H A R L G N L E F L E E
 79 K P L V G E A L A R V K R A E K K W R D K R E K L E W E T N
 80 I V Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M
 I H A A D K R V H S I R E A Y L P E L S V I P G V N A A I F
 E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S
 C W N V K G H V D V E E Q N N Q R S V L V V P E W E A E V S
 Q E V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H
 E I E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y
 T V N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S
 V Y E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V
 G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D
 S V E L L L M E E .

1 23. A pesticidal composition, according to claim
 2 12, wherein said gene, denoted pACB-1, encoding a
 3 chimeric toxin, is as follows:

4 (start HD-73) ATG GATAACAATC 400
 5 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 6 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTACACCC CAATCGATAT 500
 7 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
 8 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
 9 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT
 10 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGAAGTAAAGCA 700
 11 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
 12 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
 13 CAGTGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
 14 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
 15 TTGAGAGATG TTTCAGTGTT TGGACAAAGG TGGGGATTTG ATGCCGCGAC

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66 CTTCCGGAAT GGGGAAGCAGA AGTGTACAAA GAAGTTCGTG TCTGTCCGGG 3600
 67 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 68 GTTGCCTAAC CATTTCATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 69 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 70 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 71 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TCGTCAATC
 72 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 73 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 74 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 75 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 76 GGAA (end HD-1)

77 and equivalent nucleotide sequences coding for toxin
 78 ACB-1 with the following amino acid sequence:

79 MDNPNPINECIPYNCLSNPEVEVVLGGERIE
 80 TGYTPIDISLSLTQFLLSEFVPGAGFVLGL
 81 VDIIWGIFGPSQWDAFLVQIEQLINQRIEE
 82 FARNQAISRLEGLSNLYQIYAESFREWEAD
 83 PTNPALREEMRIQFNDMNSALTTAIPLFAV
 84 QNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
 85 RWGFDAAATINSRYNDLTRLIGNYTDYAVRW
 86 YNTGLERVWGPDSRNDWVRYNQFRRELTTLTV
 87 LDIVALFPNYDSRRYPPIRTVSQLTREIYTN
 88 PVLENFDDG⁻SFRGSAQGIERSIRSPHLM DIL
 89 NSITIIYTD AHRGYYYWSGHQIMASPVGFSG
 90 PEFTFPLYGTMGNAAPQQRIVAQLGGGVYR
 91 TLSSTLYRRPFNIGINNQQLSVLDGTEFAY
 92 GTSSNLP S AVYRKSGTVDSLNEIPPQNNNV
 93 PPRQEF SHRLSHVSMFRSGFSNS SVS IIRA
 94 PTFSSWQHRS AEFNNIIIPSSQITQIPLTKST
 95 NLGSGT SVVKGP GFTGGDILRRTSPGQIST
 96 LRVNITAPLSQR YRVRI RYASTTNLQFHTS
 97 IDGRFINQGNFSATMS SSGSNLQSGSFRTVG
 98 FTTFFNF SNGSSVFTLSAHVFNSGNEVYID
 99 RIEFVPAEVTFEAEYDLERAQKAVNELFTS
 100 SNQIGLKTDVTDYHIDQVSNLVECLSD EFC
 101 LDEKQELSEKVKHAKRLSDERNLLQDPNFR
 102 GINRQLDRGWRGSTDITIQGGDDVFKENYV
 103 TLLGTFDECYPT YLYQKIDESK LKAYTRYQ
 104 LRGYIEDS QDLEIYLIRYN AKHETVNVPGT
 105 GSLWFLSAQSP I GKC GEFNRCAPHLEWNP D
 106 LDCSCR DGEKCAHHS HHFSLDIDVGC TDLN
 107 EDLG V W V I F K I K T Q D G H A R L G N L E F L E E K P
 108 LVGEALARVKRAEKKWRDKREKLEWETNIV
 109 YKEAKESVDALFVNSQYDQLQADTNIA MIH
 110 AADKRVHSIREAYLPELSVIPGVNA AIFEE

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111 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
112 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
113 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
114 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
115 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
116 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
117 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
118 E L L L M E E .

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24. A pesticidal composition, according to
claim 12, wherein said gene, denoted pSYW1, encoding
a chimeric toxin, is as follows:

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1
2
3
4          (start HD-73)          ATG GATAACAATC 400
5 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
6 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTACACCC CAATCGATAT 500
7 TTCTTTGTCT CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
8 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
9 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAGAAT
10 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGAATAAGCA 700
11 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
12 ACTAATCCAG CATTAAAGAG AGAGATGCGT ATTCATTCA ATGACATGAA 800
13 CAGTGCCCTT ACAACCGCTA TTCTCTTTT TGCAGTTCAA AATTATCAAG
14 TTCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
15 TTGAGAGATG TTTAGTGTG TGGACAAAGG TGGGGATTTG ATGCCGCGAC
16 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
17 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
18 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
19 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
20 ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
21 GTATTAGAAA ATTTTGATGG TAGTTTTTCA GGCTCGGCTC AGGGCATAGA
22 AGGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
23 TCTATACGGA TGCTCATAAA GGGGAATATT ATTGGTCAGG GCATCAAATA
24 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCT TTCCGCTATA 1400
25 TGGAAGTATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
26 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
27 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAAAT
28 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
29 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
30 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTCGTTT 1700
31 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
32          (start HD-1)          CCAACGT TTTCTTGGCA GCATCGCAGT 1900
33 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
34 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
35 GATTTACAGG AGGAGATATT CTTCAAGAG CTTACCTGG CCAGATTTCA
36 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
37 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCATACA TCAATTGACG
38 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200
39 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
40 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
41 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA

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42 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 43 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAACAGAT GTGACGGATT
 44 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTTATC AGATGAATTT 2500
 45 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 46 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600
 47 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 48 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 49 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 50 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 51 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 52 TGTGCCAGGT ACGGGTTCCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900
 53 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 54 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000
 55 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 56 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 57 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 58 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 59 TGAATGGA AACAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 60 GCTTTATTTG TAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 61 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 62 ATCTGCCTGA GCTGTCTGTG ATTCGGGGTG TCAATGCGGC TATTTTGTGA 3400
 63 GAATTAGAAG GGCSTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 64 TGTCATTAAG AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 65 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGTG
 66 CTTCCGGAAT GGGAAGCAGA AGTGTCAACA GAAGTTCGTG TCTGTCCGGG 3600
 67 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 68 GTTGCCTAAC CATTATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 68 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 70 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 71 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TCGTCACTC
 72 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 73 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 74 AAGAATTAGA ATACTTCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 75 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAAATTAC TCCTTATGGA
 76 GGAA (end HD-1)

77 and equivalent nucleotide sequences coding for toxin
 78 SYW1 with the following amino acid sequence:

79 M D N N F N I N E C I P Y N C L S N P E V E V L G G E R I E
 80 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
 81 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
 82 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
 83 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
 84 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
 85 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 86 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
 87 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
 88 P V L E N F D G S F R G S A Q G I E G S I R S P H L M D I L
 89 N S I T I Y T D A H K G E Y Y W S G H Q I M A S P V G F S G
 90 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R

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91 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
 92 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V
 93 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
 94 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
 95 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
 96 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
 97 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
 98 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
 99 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
 100 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
 101 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
 102 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
 103 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
 104 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
 105 G S L W P L S A Q S P I G K C G E F N R C A P H L E W N P D
 106 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
 107 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
 108 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
 109 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
 110 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
 111 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
 112 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
 113 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
 114 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
 115 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
 116 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
 117 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
 118 E L L L M E E .

1 25. A recombinant DNA transfer vector comprising
 2 DNA having the following nucleotide sequence or
 3 equivalent nucleotide sequences containing bases whose
 4 translated region codes for the same amino acid sequence:

5 (start HD-73) ATG GATAACAATC 400
 6 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 7 GAAGTATTAG GTGGAGAAAG AATAGAACT GGTTACACCC CAATCGATAT 500
 8 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
 9 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
 10 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT
 11 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGAATAAGCA 700
 12 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
 13 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCATTCA ATGACATGAA 800
 14 CAGTGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
 15 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
 16 TTGAGAGATG TTTCASTGTT TGGACAAAGG TGGGGATTTG ATGCCGCGAC
 17 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
 18 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 19 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACT 1100
 20 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
 21 ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
 22 GTATTAGAAA ATTTTGATGG TAGTTTTCSA GGCTCGGCTC AGGGCATAGA

23 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 24 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA
 25 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCT TTCCGCTATA 1400
 26 TGGAACTATG GGAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
 27 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 28 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 29 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 30 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
 31 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTCGTTC 1700
 32 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 33 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900
 34 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 35 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
 36 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTTCA
 37 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 38 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
 39 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200
 40 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
 41 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 42 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAAGTA
 43 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 44 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAACAGAT GTGACGGATT
 45 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTTATC AGATGAATTT 2500
 46 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 47 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600
 48 ATAGACAACCT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 49 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 50 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 51 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 52 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 53 TGTGCCAGGT ACGGGTTTCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900
 54 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 55 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000
 56 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 57 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 58 CTAGGGAAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 59 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 60 TGBAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 61 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 62 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 63 ATCTGCCTGA GCTGTCTGTG ATTCGGGGTG TCAATGCGGC TATTTTGA 3400
 64 GAATTAGAAG GCGTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 65 TGTCATTAAG AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 66 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGTG
 67 CTTCCGGAAT GGGAGCAGA AGTGTCACAA GAAGTTCGTG TCTGTCCGGG 3600
 68 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 69 GTTGCGTAAC CATTATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 70 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 71 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTGTAA 3800
 72 ATCGAGGATA TAACGAAGCT CTTTCCGTAC CAGCTGATTA TGCCTAGTC
 73 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 74 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 75 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 76 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 77 GGAA (end HD-1).

26. A recombinant DNA transfer vector comprising
DNA having the following nucleotide sequence or
equivalent nucleotide sequences containing bases whose
translated region codes for the same amino acid sequence:

```

      (start HD-1)          ATGG ATAACAATCC GAACATCAAT
6   GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
7   TGGAGAAAGA ATAGAAACTG GTTACACCCC AATCGATATT TCCTTGTCGC
8   TAACGCAATT TCTTTTGAGT GAATTTGTTT CCGGTGCTGG ATTTGTGTTA 700
9   GGACTAGTTG ATATAATATG GGGGAATTTT GGTCCCTCTC AATGGGACGC
10  ATTTCTGTGA CAAATTGAAC AGTTAATTAA CCAAAGAATA GAAGAATTCTG 800
11  CTAGGAACCA AGCCATTTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA
12  ATTTACGCAG AATCTTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900
13  ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA
14  CAACCGCTAT TCCTCTTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTTA 1000
15  TCAGTATATG TTCAAGCTGC AAATTTACAT TTATCAGTTT TGAGAGATGT
16  TTCAGTSTTT GGACAAAGST GGGGATTTGA TGCCGCGACT ATCAATAGTC 1100
17  GTTATAATGA TTTAACTAGG CTTATTGGCA ACTATACAGA TTATGCTGTG
18  CGCTGGTACA ATACGGGATT AGAGCGTGTA TGGGGACCGG ATTCTAGAGA 1200
19  TTGGGTAAGG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG
20  ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTCGA 1300
21  ACAGTTTCCC AATTAACAAG AGAAATTTAT ACGAACCCAG TATTAGAAAA
22  TTTTGATGGT AGTTTTCTGT GAATGGCTCA GAGAATAGAA CAGAATATTA 1400
23  GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCAT TTATACTGAT
24  GTGCATAGAG GCTTTAATTA TTGGTCAGGG CATCAAATAA CAGCTTCTCC 1500
25  TGTAGGGTTT TCAGGACCAG AATTCGCATT CCCTTTATTT GGGAAATGCGG
26  GGAATGCAGC TCCACCCGTA CTTGTCTCAT TAACTGGTTT GGGGATTTTT 1600
27  AGAACATTAT CTTACCTTTT ATATAGAAGA ATTATACTTG GTTCAGGCCC
28  AAATAATCAG GAAGTGTGTT TCCTTGATGG AACGGAGTTT TCTTTTGCC 1700
29  CCTAACGAC CAAGTTGCC TCCACTATAT ATAGACAAAG GGGTACAGTC
30  GATTCAGTAG ATGTAATACC GCCACAGGAT AATAGTGTAC CACCTCGTGC 1800
31  GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
32  GAGCAGTTTA CACCTTGAGA GCTCAACGT (stop HD-1)
      (start HD-73)          CCT ATGTTCTCTT
33  GGATACATCG TAGTGCTGAA TTTAATAATA TAATTGCATC GGATAGTATT 1800
34  ACTCAAATCC CTGCAGTGAA GGGAAACTTT CTTTTTAATG GTTCTGTAAT
35  TTCAGGACCA GGATTTACTG GTGGGGACTT AGTTAGATTA AATAGTAGTG 1900
36  GAAATAACAT TCAGAATAGA GGGTATATTG AAGTTCCAAT TCACTTCCCA
37  TCGACATCTA CCAGATATCG AGTTCGTGTA CGGTATGCTT CTGTAACCCC 2000
38  GATTCACCTC AACGTTAATT GGGGTAATTC ATCCATTTTT TCCAATACAG
39  TACCAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTTGGT 2100
40  TATTTTGAAG GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG
41  TGTTAGAAAT TTTAGTGGGA CTGCAGGAGT GATAATAGAC AGATTTGAAT 2200
42  TTATTCCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG
43  CAGAAGGCGG TGAATGCGCT GTTTACGTCT ACAAACCAAC TAGGGCTAAA 2300
44  AACAAATGTA ACGGATTATC ATATTGATCA AGTGTTCCAAT TTAGTTACGT
45  ATTTATCGGA TGAATTTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
46  GTCAAACATG CGAAGCGACT CAGTGATGAA CGCAATTTAC TCCAAGATTC
47  AAATTTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCAGGAAGTA 2500
48  CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAGAA AAATTACGTC
49  ACACTATCAG GTACCTTTGA TGAGTGCTAT CCAACATATT TGTATCAAAA 2600
50  AATCGATGAA TCAAAATTAA AAGCCTTTAC CCGTTATCAA TTAAGAGGGT

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52 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTCTG CTACAATGCA 2700
 53 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCTTAT GGCCGCTTTC
 54 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCBCGCCAC 2800
 55 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAG
 56 TGTGCCCATC ATTCGCATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900
 57 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC
 57 AAGATGGGCA CGCAAGACTA GGGAACTAG AGTTTCTCGA AGAGAAACCA 3000
 59 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG
 60 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAGAGG 3100
 61 CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATCAATTA
 62 CAAGCGGATA CGAATATTGC CATGATTCAT GCGGCAGATA AACGTGTTCA 3200
 63 TAGCATTGCA GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA
 64 ATGCGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTTCAC TGCATTCTCC 3300
 65 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTTTA ATAATGGCTT
 66 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400
 67 AACGTTGCGT CCTTGTGTGT CCGGAATGGG AAGCAGAAAT GTCACAAGAA
 68 GTTCGTGTCT GTCCGGGTCT TGGCTATATC CTTCGTGTCA CAGCGTACAA 3500
 69 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA
 70 CAGACGAACT GAAGTTTAGC AACTGCGTAG AAGAGGAAAT CTATCCAAT 3600
 71 AACACGATAA CGTGAATGA TTATACTGTA AATCAGAAAG AATACGGAGG
 72 TGCGTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAG 3700
 73 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA
 74 GAGAATCCTT GTGAATTTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800
 75 AGTTGGTTAT GTGACAAAAG AATTAGAATA CTTCCAGAA ACCGATAAGG
 76 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTTATCGT GGACAGCGTG 3900
 77 GAATTACTCC TTATGGAGGA A (end HD-73).

1 27. A recombinant DNA transfer vector comprising
 2 DNA having the following nucleotide sequence or
 3 equivalent nucleotide sequences containing bases whose
 4 translated region codes for the same amino acid
 5 sequence:

6 (start HD-73) ATG GATAACAATC 400
 7 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 8 GAAGTATTAG GTGGAGAAAG AATAGAACT GGTACACCC CAATCGATAT 500
 9 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
 10 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
 11 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAGAAT
 12 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGACTAAGCA 700
 13 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
 14 ACTAATCCAG CATTAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
 15 CAGTGCCCTT ACAACCGCTA TTCTCTTTT TGCAGTTCAA AATTATCAAG
 16 TTCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
 17 TTGAGAGATG TTTAGTGTG TGGACAAAGG TGGGGATTG ATGCCGCGAC
 18 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
 19 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 20 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
 21 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT

22	ATCCAATTCG	AACAGTTTCC	CAATTAACAA	GAGAAATTTA	TACAAACCCA	1200
23	GTATTAGAAA	ATTTTGATGG	TAGTTTTCSA	GGCTCGGCTC	AGGGCATAGA	
24	AAGAAGTATT	AGGAGTCCAC	ATTTGATGGA	TATACTTAAC	AGTATAACCA	1300
25	TCTATACGGA	TGCTCATAGG	GGTTATTATT	ATTGGTCAGG	GCATCAAATA	
26	ATGGCTTCTC	CTGTAGGGTT	TTCGGGGCCA	GAATTCACTT	TTCCGCTATA	1400
27	TGGAACATATG	GGAAATGCAG	CTCCACAACA	ACGTATTGTT	GCTCAACTAG	
28	GTCAGGGCGT	GTATAGAACA	TTATCGTCCA	CTTTATATAG	AAGACCTTTT	1500
29	AATATAGGGA	TAAATAATCA	ACAACATCT	GTTCTTGACG	GGACAGAATT	
30	TGCTTATGGA	ACCTCCTCAA	ATTTGCCATC	CGCTGTATAC	AGAAAAAGCG	1600
31	GAACGGTAGA	TTCGCTGAAT	GAAATACCGC	CACAGAATAA	CAACGTGCCA	
32	CCTAGGCAAG	AATTTAGTCA	TCGATTAAGC	CATGTTTCAA	TGTTTCGTTC	1700
33	AGGCTTTAGT	AATAGTAGTG	TAAGTATAAT	AAGAGCT (end	hd-73)	
34	(start	HD-1)	CCAACGT	TTTCTTGGCA	GCATCGCAGT	1900
35	GCTGAATTTA	ATAATATAAT	TCCTTCATCA	CAAATTACAC	AAATACCTTT	
36	AACAAAATCT	ACTAATCTTG	GCTCTGGAAC	TTCTGTGCTT	AAAGGACCAG	2000
37	GATTTACAGG	AGGAGATATT	CTTCGAAGAA	CTTCACCTGG	CCAGATTTCA	
38	ACCTTAAGAG	TAAATATTAC	TGCACCATTA	TCACAAAGAT	ATCGGGTAAG	2100
39	AATTCGCTAC	GCTTCTACTA	CAAATTTACA	ATTCCATACA	TCAATTGACG	
40	GAAGACCTAT	TAATCAGGGT	AATTTTTTCA	CAACTATGAG	TAGTGGGAGT	2200
41	AATTTACAGT	CCGGAGGCTT	TAGGACTGTA	GGTTTTACTA	CTCCGTTTAA	
42	CTTTTCAAAT	GGATCAAGTG	TATTTACGTT	AAGTGCTCAT	GTCTTCAATT	2300
43	CAGGCAATGA	AGTTTATATA	GATCGAATTG	AATTTGTTCC	GGCAGAAGTA	
44	ACCTTTGAGG	CAGAATATGA	TTTAGAAAGA	GCACAAAAGG	CGGTGAATGA	2400
45	GCTGTTTACT	TCTTCCAATC	AAATCGGGTT	AAAAACAGAT	GTGACGGATT	
46	ATCATATTGA	TCAAGTATCC	AATTTAGTTG	AGTGTTTATC	AGATGAATTT	2500
47	TGTCTGGATG	AAAAACAAGA	ATTGTCCGAG	AAAGTCAAAC	ATGCGAAGCG	
48	ACTTAGTGAT	GAGCGGAATT	TACTTCAAGA	TCCAACTTC	AGAGGGATCA	2600
49	ATAGACAACT	AGACCGTGSC	TGGAGAGGAA	GTACGGATAT	TACCATCCAA	
50	GGAGGCGATG	ACGTATTCAA	AGAGAATTAC	GTTACGCTAT	TGGGTACCTT	2700
51	TGATGAGTGC	TATCCAACGT	ATTTATATCA	AAAAATAGAT	GAGTCGAAAT	
52	TAAAAGCCTA	TACCCGTTAT	CAATTAAGAG	GGTATATCSA	AGATAGTCAA	2800
53	GACTTAGAAA	TCTATTTAAT	TCGCTACAAT	GCAAAACATG	AAACAGTAAA	
54	TGTGCCAGGT	ACGGGTTCCCT	TATGGCCGCT	TTGAGCCCAA	AGTCCAATCG	2900
55	GAAAGTGTGG	AGAGCCGAAT	CGATGCGCGC	CACACCTTGA	ATGGAATCCT	
56	GACTTAGATT	GTTCGTGTAG	GGATGGAGAA	AAGTGTGCCC	ATCATTGCGA	3000
57	TCATTTCTCC	TTAGACATTG	ATGTAGGATG	TACAGACTTA	AATGAGGACC	
58	TAGGTGTATG	GGTGATCTTT	AAGATTAAGA	CGCAAGATGG	GCACGCAAGA	3100
59	CTAGGGAATC	TAGAGTTTCT	CGAAGAGAAA	CCATTAGTAG	GAGAAGCGCT	
60	AGCTCGTGTG	AAAAGAGCGG	AGAAAAAATG	GAGAGACAAA	CGTGAAAAAT	3200
61	TGSAATGGGA	AACAAATATC	GTTTATAAAG	AGGCAAAAGA	ATCTGTAGAT	
62	GCTTTATTTG	TAAACTCTCA	ATATGATCAA	TTACAAGCGG	ATACGAATAT	3300
63	TGCCATGATT	CATGCGGCAG	ATAAACGTGT	TCATAGCATT	CGAGAAGCTT	
64	ATCTGCCTGA	GCTGTCTGTG	ATTCCGGGTG	TCAATGCGGC	TATTTTTGAA	3400
65	GAATTAGAAG	GGCGTATTTT	CACTGCATTC	TCCCTATATG	ATGCGAGAAA	
66	TGTCATTAAA	AATGGTGATT	TTAATAATGG	CTTATCCTGC	TGGAACGTGA	3500
67	AAGGGCATGT	AGATGTAGAA	GAACAAAACA	ACCAACGTTT	GGTCCTTGTT	
68	CTTCCGGAAT	GGGAAGCAGA	AGTGTACAAA	GAAGTTCGTG	TCTGTCCGGG	3600
69	TCGTGGCTAT	ATCCTTCGTG	TCACAGCGTA	CAAGGAGGGA	TATGGAGAAG	
70	GTTGCGTAAC	CATTCATGAG	ATCGAGAACA	ATACAGACGA	ACTGAAGTTT	3700
71	AGCAACTGCG	TAGAAGAGGA	AATCTATCCA	AATAACACGG	TAACGTGTAA	

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72 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 73 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TCGTCAATC
 74 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 75 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 76 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 77 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 78 GGAA (end HD-1).

1 28. A recombinant DNA transfer vector comprising
 2 DNA having the following nucleotide sequence or
 3 equivalent nucleotide sequences containing bases whose
 4 translated region codes for the same amino acid
 5 sequence:

6 (start HD-73) ATG GATAACAATC 400
 7 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 8 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTTACACCC CAATCGATAT 500
 9 TTCCTTGTCT CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGTCT
 10 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGSTCCCTCT 600
 11 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT
 12 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGAATAAGCA 700
 13 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
 14 ACTAATCCAG CATTAGAGAG AGAGATGCGT ATTCATTCA ATGACATGAA 800
 15 CAGTGCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
 16 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
 17 TTGAGAGATG TTTCASTGTT TGGACAAAGG TGGGGATTTG ATGCCGCGAC
 18 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
 19 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 20 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTAGAGAGAG AATTAACACT 1100
 21 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
 22 ATCCAATTCT AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
 23 GTATTAGAAA ATTTTGTATG TAGTTTTTCA GGCTCGGCTC AGGGCATAGA
 24 AGGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 25 TCTATACGGA TGCTCATAAA GGGGAATATT ATTGGTCAGG GCATCAAATA
 26 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCT TTCCGCTATA 1400
 27 TGGAACATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
 28 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 29 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAAAT
 30 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 31 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
 32 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTTCGTTT 1700
 33 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 34 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900
 35 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 36 AACAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
 37 GATTTACAGG AGGAGATATT CTTGGAAGAA CTTACCTGG CCAGATTTC
 38 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 39 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCATACA TCAATTGACG

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40 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200
 41 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
 42 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 43 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
 44 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 45 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAACAGAT GTGACGGATT
 46 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTTATC AGATGAATTT 2500
 47 TGTCTGAGTG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 48 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
 49 ATAGACAACCT AGACCGTGCG TGGAGAGGAA GTACGGATAT TACCATCCAA
 50 GGAAGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 51 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 52 TAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 53 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 54 TGTGCCAGGT ACGGGTTCCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900
 55 GAAAGTGTGG AGAGCCGAAT CGATGCGCSC CACACCTTGA ATGGAATCCT
 56 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000
 57 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 58 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 59 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 60 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 61 TGAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 62 GCTTTATTTG TAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 63 TGCCATGATT CATGCGGCGA ATAAACGTGT TCATAGCATT CGAGAAGCTT
 64 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGA 3400
 65 GAATTAGAGG GGCATATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 66 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 67 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT
 68 CTTCCGGAAT GGGGAAGCAGA AGTGTACAAA GAAGTTCTGT TCTGTCCGGG 3600
 69 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 70 GTTGCCTAAC CATTCATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 71 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 72 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 73 ATCGAGGATA TAACGAAGCT CTTCCGTAC CAGCTGATTA TGCCTCAGTC
 74 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 75 TAACAGAGGG TATAGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 76 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 77 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 78 GGAA (end HD-1).

1 29. The DNA transfer vector of claim 25 trans-
 2 ferred to and replicated in a prokaryotic or lower
 3 eukaryotic microorganism.

1 30. The DNA transfer vector of claim 26 trans-
2 ferred to and replicated in a prokaryotic or lower
3 eukaryotic microorganism.

1 31. The DNA transfer vector of claim 27 trans-
2 ferred to and replicated in a prokaryotic or lower
3 eukaryotic microorganism.

1 32. The DNA transfer vector of claim 28 trans-
2 ferred to and replicated in a prokaryotic or lower
3 eukaryotic microorganism.

1 33. Plasmid pEW1 as shown in FIGURE 1 of the
2 drawings.

1 34. Plasmid pEW2 as shown in FIGURE 2 of the
2 drawings.

1 35. Plasmid pEW3 as shown in FIGURE 3 of the
2 drawings.

1 36. Plasmid pEW4 as shown in FIGURE 4 of the
2 drawings.

1 37. Plasmid pACB-1, having the construction of
2 plasmid pEW3 except that the DNA encoding aspartic
3 acid at position 411 is converted to encode asparagine,
4 and the DNA encoding glycine at position 425 is con-
5 verted to encode glutamic acid.

1 38. Plasmid pSYW1, having the construction of plasmid
2 pEW3 except that the DNA encoding arginine at position
3 289 is converted to encode glycine, the DNA encoding
4 arginine at position 311 is converted to encode lysine,
5 and the DNA encoding tyrosine at position 313 is conver-
6 ted to encode glutamate.

1 39. A microorganism transformed by the transfer
2 vector of claim 25.

1 40. A microorganism transformed by the transfer
2 vector of claim 26.

1 41. A microorganism transformed by the transfer
2 vector of claim 27.

1 42. A microorganism transformed by the transfer
2 vector of claim 28.

1 43. E. coli (pEW3), a microorganism according
2 to claim 39.

1 44. E. coli (pEW4), a microorganism according to
2 claim 40.

1 45. E. coli (pACB-1), a microorganism according
2 to claim 41.

1 46. E. coli (pSYW1), a microorganism according
2 to claim 42.

1 47. A process for preparing pesticidal chimeric
2 toxin EW3 having the following amino acid sequence:

3 MDNNPNINEDCIPYNCLSNP E V E V L G G E R I E
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
5 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
8 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
11 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
12 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
13 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G

14 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
16 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V
17 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
18 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
19 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
20 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
21 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
23 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
24 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
26 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
27 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
29 G S L W P L S A Q S P I G K C G E F N R C A P H L E W N P D
30 L D C S C R D G E K C A H H S H F S L D I D V G C T E D L N
31 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
33 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
36 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
37 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
39 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
42 E L L L M E E

43 which comprises culturing a prokaryotic microbe
44 hosting a recombinant DNA transfer vector, denoted
45 pEW3, comprising DNA having the following nucleotide
46 sequence or equivalent nucleotide sequences containing
47 bases whose translated region codes for the same
48 amino acid sequence:

49 (start HD-73) ATG GATAACAATC 400
50 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
51 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTTACACCC CAATCGATAT 500
52 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
53 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
54 CAATGGGACG CATTTCCTGT ACAAAATTGAA CAGTTAATTA ACCAAAGAAT
55 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGAATAAGCA 700
56 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
57 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCATTCA ATGACATGAA 800
58 CAGTGGCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
59 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
60 TTGAGAGATG TTTAGTGTT TGGACAAAGG TGGGGATTG ATGCCGCGAC

61	TATCAATAGT	CGTTAATAAT	ATTTAAGTAG	GCTTATTGGC	AACATACAG	1000
62	ATTATGCTGT	ACGCTGGTAC	AATACGGGAT	TAGAACGTGT	ATGGGGACCG	
63	GATTCTAGAG	ATTGGGTAAG	GTATAATCAA	TTTAGAAGAG	AATTAACACT	1100
64	AACTGTATTA	GATATCGTTG	CTCTGTTCCC	GAATTATGAT	AGTAGAAGAT	
65	ATCCAATTCG	AACAGTTTCC	CAATTAACAA	GAGAAATTTA	TACAAACCCA	1200
66	GTATTAGAAA	ATTTTGATGG	TAGTTTTCSA	GGCTCGGCTC	AGGGCATAGA	
67	AAGAAGTATT	AGGAGTCCAC	ATTTGATGGA	TATACTTAAC	AGTATAACCA	1300
68	TCTATACGGA	TGCTCATAGG	GGTTATTATT	ATTGGTCAGG	GCATCAAATA	
69	ATGGCTTCTC	CTGTAGGGTT	TTGGGGGCCA	GAATTCACCT	TTCCGCTATA	1400
70	TGGAAGTATG	GGAAATGCAG	CTCCACAACA	ACGTATTGTT	GCTCAACTAG	
71	GTCAGGGCGT	GTATAGAACA	TTATCGTCCA	CTTTATATAG	AAGACCTTTT	1500
72	AATATAGGGA	TAAATAATCA	ACAACTATCT	GTTCTTGACG	GGACAGAATT	
73	TGCTTATGGA	ACCTCCTCAA	ATTTGCCATC	CGCTGTATAC	AGAAAAAGCG	1600
74	GAACGGTAGA	TTGCTGCGAT	GAAATACCGC	CACAGAATAA	CAACGTGCCA	
75	CCTAGGCAAG	GATTTAGTCA	TCGATTAAGC	CATGTTTCAA	TGTTTCGTTT	1700
76	AGGCTTTAGT	AATAGTAGTG	TAAGTATAAT	AAGAGCT (end	hd-73)	
77	(start	HD-1)	CCAACGT	TTTCTTGCCA	GCATCGCAGT	1900
78	GCTGAATTTA	ATAATATAAT	TCCTTCATCA	CAAATTACAC	AAATACCTTT	
79	AACAAAATCT	ACTAATCTTG	GCTCTGGAAC	TTCTGTCGTT	AAAGGACCAG	2000
80	GATTTACAGG	AGGAGATATT	CTTCGAAGAA	CTTCACCTGG	CCAGATTTCA	
81	ACCTTAAGAG	TAAATATTAC	TGCACCATTA	TCACAAAGAT	ATCGGGTAAG	2100
82	AATTCGCTAC	GCTTCTACTA	CAAATTTACA	ATTCCATACA	TCAATTGACG	
83	GAAGACCTAT	TAATCAGGGT	AATTTTTTCA	CAACTATGAG	TAGTGGGAGT	2200
84	AATTTACAGT	CCGGAGGCTT	TAGGACTGTA	GGTTTTACTA	CTCCGTTTAA	
85	CTTTTCAAAT	GGATCAAGTG	TATTTACGTT	AAGTGCTCAT	GTCTTCAATT	2300
86	CAGGCAATGA	AGTTTATATA	GATCGAATTG	AATTTGTTCC	GGCAGAAAGT	
87	ACCTTTGAGG	CAGAATATGA	TTTAGAAAGA	GCACAAAAGG	CGGTGAATGA	2400
88	GCTGTTTACT	TCTTCCAATC	AAATCGGGTT	AAAAACAGAT	GTGACGGATT	
89	ATCATATTGA	TCAAGTATCC	AATTTAGTTG	AGTGTTTATC	AGATGAATTT	2500
90	TGCTCTGGATG	AAAAACAAGA	ATTGTCCGAG	AAAGTCAAAC	ATGCGAAGCG	
91	ACTTAGTGAT	GAGCGGAATT	TACTTCAAGA	TCCAAACTTC	AGAGGGATCA	2600
92	ATAGACAAC	AGACCGTGGC	TGGAGAGGAA	GTACGGATAT	TACCATCCAA	
93	GGAGGGCGATG	ACGTATTCAA	AGAGAATTAC	GTTACGCTAT	TGGGTACCTT	2700
94	TGATGAGTGC	TATCCAACGT	ATTTATATCA	AAAAATAGAT	GAGTCGAAAT	
95	TAAAAGCCTA	TACCCGTTAT	CAATTAAGAG	GGTATATCSA	AGATAGTCAA	2800
96	GACTTAGAAA	TCTATTTAAT	TCGCTACAAT	GCAAAACATG	AAACAGTAAA	
97	TGTGCCAGGT	ACGGGTTCC	TATGGCCGCT	TTACGCCCAA	AGTCCAATCG	2900
98	GAAAGTGTGG	AGAGCCGAAT	CGATGCGCGC	CACACCTTGA	ATGGAATCCT	
99	GACTTAGATT	GTTGCTGTAG	GGATGGAGAA	AAGTGTGCCC	ATCATTCGCA	3000
100	TCATTTCTCC	TTAGACATTG	ATGTAGGATG	TACAGACTTA	AATGAGGACC	
101	TAGGTGTATG	GGTGATCTTT	AAGATTAAGA	CGCAAGATGG	GCACGCAAGA	3100
102	CTAGGGGAATC	TAGAGTTTCT	CGAAGAGAAA	CCATTAGTAG	GAGAAAGCGCT	
103	AGCTCGTGTG	AAAAGAGCGG	AGAAAAAATG	GAGAGACAAA	CGTGAAAAAT	3200
104	TGGAATGGGA	AACAAATATC	GTTTATAAAG	AGGCAAAAGA	ATCTGTAGAT	
105	GCTTTATTTG	TAAACTCTCA	ATATGATCAA	TTACAAGCGG	ATACGAATAT	3300
106	TGCCATGATT	CATGCGGCAG	ATAACGTGT	TCATGACATT	CGAGAAGCTT	
107	ATCTGCCTGA	GCTGTCTGTG	ATTCCGGGTG	TCAATGCGGC	TATTTTTGAA	3400
108	GAATTAGAAG	GGCGTATTTT	CACCTGATTC	TCCCTATATG	ATGCGAGAAA	
109	TGTCATTAAA	AATGGTGATT	TTAATAATGG	CTTATCCTGC	TGGAACGTGA	3500
110	AAGGGCATGT	AGATGTAGAA	GAACAAAACA	ACCAACGTTT	GGTCTTGT	
111	CTTCCGGAAT	GGGAAGCAGA	AGTGTACAAA	GAAGTTCGTG	TCTGTCCGGG	3600
112	TCGTGGCTAT	ATCCTTCGTG	TCACAGCGTA	CAAGGAGGGA	TATGGAGAAG	
113	GTTGCGTAAC	CATTTCATGAG	ATCGAGAACA	ATACAGACGA	ACTGAAGTTT	3700
114	AGCAACTGCG	TAGAAGAGGA	AATCTATCCA	AATAACACGG	TAACGTGTAA	

M12C1FDF3D2

115 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 116 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC
 117 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 118 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 119 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 120 GAAACGGAAG GAACATTAT CGTGGACAGC GTGGATTAC TCCTTATGGA
 121 GGAA (end HD-1).

1 48. A process for preparing pesticidal chimeric
 2 toxin EW4 having the following amino acid sequence:

3 MDNNPNIN ECIPYNC LSNPEVEVL GGERIE
 4 TGYTPIDISLSLTQFLLSEFVPGAGFVLGL
 5 VDI IWGIFGPSQWDAFPVQIEQLINQRIEE
 6 FARNQAI SRLEG LSNLYQIYAESFREWEAD
 7 PTNPALREEMRIQFNDMNSALTTAIPLLAV
 8 QNYQVPLLSVYVQAANLHLSVLRDVS VFGQ
 9 RWGFDAATINSRYNDLTRLIGNYTDYAVRW
 10 YNTGLERVWGFDSRDWVRYNQFRRELTLTV
 11 LDIVALF SNYDSRRYP IRTVSQLTREIYTN
 12 PVLENF DGSFRGM AQRIEQNIRQPHLM DIL
 13 NSIT IYTDVHRGF NYWSGHQITASPVGFSG
 14 PEFAPFLFGNAGNAAPPVLVSLTGLGIFRT
 15 LSSPLYRR IILGSGFPNNQELFVL DGT EFSF
 16 ASLTTNLPSTIYRQRGTVDSDL DVI PPQ DNS
 17 VPPRAGF SHRLSHVTMLSQAAGAVYTLRAQ
 18 RPFMFSWIHRSAEFNNIIASDSITQIPAVKG
 19 NFLFN GSVISGPGFTGGDLVRLNSSSGNNIQ
 20 NRGYIEVP IHF PSTSTRYRV RVR YASVTPI
 21 HLN VNWGNSSIFSNTVPATATSLDNLQSSD
 22 FGYFESANAF TSSSLGNIVGV RNFSGTAGVI
 23 IDRFEFIPVTATLEAEYNLERAQKAVNALF
 24 TSTNOLGLKTNVTDYHIDQVSNLV TYLSDE
 25 FCLDEKRELSEKVKHAKRLSDERNLLQDSN
 26 FKDINRQPERGWWGGSTGITIQGGDDVFKEN
 27 YVTL SGT FDECYFTYLYQK IDESKLKAFTR
 28 YQLRGYIEDS QDLEIYLI RYN AKHETVNVP
 29 GTGSLWFLSAQSPIGKCGEPNRCAPHLEWN
 30 PDLDCSCRDG EKCAH HSHHFSLDIDV GCTD
 31 LNEDLGVWVIFKIKTQDGHARLGNLEFLEE
 32 KPLVGEALARVKRAEKKWRDKREKLEWETN
 33 IVYKEAKESVDALFVNSQYDQLQADTNIAM
 34 IHAADKRVHSIREAYLPELSVIPGVNAAIF
 35 EELEGRIFTAFSELYDARNVIKNGDFNGLS
 36 CWNVKGHV DVEEQNNQ RSVLVVPEWEAEVS
 37 QEV RVCPGRGVI LRV TAYKEGYGEGCVTIH
 38 EIENNTDELKFSNCVEEEIYPNNTVTCNDY
 39 TVNQEEYGGAYTSRN RGYNEAPSVPADYAS
 40 VYEEKSYTDGRRENPCFNRGYRDYTPLPV
 41 GYVTKELEYFPETDKVWIEIGETEGTFIVD
 42 SVELLLMEE

10035050 122701

43 which comprises culturing a prokaryotic microbe
44 hosting a recombinant DNA transfer vector, denoted
45 pEW4, comprising DNA having the following nucleotide
46 sequence or equivalent nucleotide sequences containing
47 bases whose translated region codes for the same amino
48 acid sequence:

49 (start HD-1) ATGG ATAACAATCC GAACATCAAT
50 GAATGCATTCTTATAATTGTTAAGTAACCTGAAGTAGAGTATTAGG 600
51 TGGAGAAAGAATAGAACTGTTACACCCC AATCGATATTTCCTTGTCGCG
52 TAACGCAATTCTTTTGAGTGAATTTGTTCCGGTGCTGGATTTGTGTTA 700
53 GGACTAGTTGATATAATATGGGAATTTTTGGTCCCTCTCAATGGGACGCG
54 ATTTCTGTGTA CAAATTGAACAGTTAATTAA CCAAGAATA GAAGAATTCTG 800
55 CTAGGAACCAAGCCATTTCTAGATTAGAAGGACTAAGCAA TCTTTATCAA
56 ATTTACGCAGATCTTTTAGAGAGTGGGAA GCAGATCCTA CTAATCCAGC 900
57 ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA
58 CAACCGCTATTCCTCTTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTTA 1000
59 TCAGTATATGTTCAAGCTGC AAATTTACAT TTATCAGTTT TGAGAGATGT
60 TTCAGTGTTTGGACAAAGGTGGGGATTTGATGCCGCGACTATCAATAGTC 1100
61 GTTATAATGATTTAACTAGGCTTATTGGCA ACTATACAGA TTATGCTGTG
62 CGCTGGTACAATACGGGATTAGAGCGTGTA TGGGGACCGGATTCTAGAGA 1200
63 TTGGGTAAGGTATAATCAATTTAGAAGAGA GCTAACACTTACTGTATTAG
64 ATATCGTTGCTCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTCGA 1300
65 ACAGTTTCCC AATTAACAAGAGAAATTTATACGAACCCAGTATTAGAAAA
66 TTTTGATGGTAGTTTTCTGTGGAATGGCTCAGAGAATAGAA CAGAATATTA 1400
67 GGCAACCACATCTTATGGATATCCTTAATA GTATAACCATTTATACTGAT
68 GTGCATAGAGGCTTTAATTA TTGGTCAGGGCATCAATAA CAGCTTCTCC 1500
69 TGTAGGGTTTTCAGGACCAG AATTCGCATTCCCTTTATTTGGGAATGCGG
70 GGAATGCAGCTCCACCCGTA CTTGTCTCATTAAGTGGTTTGGGGATTTTT 1600
71 AGAACATTATCTTCACCTTTATATAGAAGA ATTATACTTG GTTCAGGCCC
72 AAATAATCAGGAAGTGTGTTCTCTTGATGG AACGGAGTTTCTTTTTGCCT 1700
73 CCCTAACGACCAACTTGCTTCCACTATATATAGACAAAGGGGTACAGTC
74 GATTCACTAGATGTAATACC GCCACAGGATAATAGTGTAC CACCTCGTGC 1800
75 GGGATTTAGCATCGATTGAGTCATGTTAC AATGCTGAGC CAAGCAGCTG
76 GAGCAGTTTACACCTTGAGA GCTCAACGT (stop HD-1)
77 (start HD-73) CCT ATGTTCTCTT
78 GGATACATCGTAGTGCTGAA TTTAATAATA TAATTGCATC GGATAGTATT 1800
79 ACTCAAATCCCTGCAGTGAA GGGAACTTTCTTTTAATG GTTCTGTAA
80 TTCAGGACCA GGATTTACTG GTGGGGACTT AGTTAGATTA AATAGTAGTG 1900
81 GAAATAACATTCAGAATAGA GGGTATATTG AAGTTCCAAT TCACTTCCCA
82 TCGACATCTA CCAGATATCG AGTTCGTGTA CGGTATGCTTCTGTAACCCC 2000
83 GATTACCTCAACGTTAATTGGGGTAATTCATCCATTTTTTCCAATACAG
84 TACCAGCTACAGCTACGTCA TTAGATAATCTACAATCAAGTGATTTTGGT 2100
85 TATTTTGAAGTGCCCAATGCTTTTACATCTTCATTAGGTA ATATAGTAGG
86 TGTTAGAAATTTAGTGGGACTGCAGGAGTGATAATAGACAGATTTGAAT 2200
87 TTATTCCAGT TACTGCAACA CTCGAGGCTG AATATAATCTGGAAAGAGCG

88 CAGAAGGCGG TGAATGCGCT GTTTACGTCT ACAAACCAAC TAGGGCTAAA 2300
 89 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT
 90 ATTTATCGGA TGAATTTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
 91 GTCAAACATG CGAAGCGACT CAGTGATGAA CGCAATTTAC TCCAAGATTG
 92 AAATTTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCGBAAGTA 2500
 93 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAGA AAATTACGTC
 94 ACACTATCAG GTACCTTTGA TGAGTGCTAT CCAACATATT TGTATCAAAA 2600
 95 AATCGATGAA TCAAAATTAA AAGCCTTTAC CCGTTATCAA TTAAGAGGGT
 96 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTG CTACAATGCA 2700
 97 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCCTTAT GGCCGCTTTC
 98 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCGCGCCAC 2800
 99 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAG
 100 TGTGCCCATC ATTCGCATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900
 101 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC
 102 AAGATGGGCA CGCAAGACTA GGGAACTAG AGTTTCTCGA AGAGAAACCA 3000
 103 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG
 104 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAAGAGG 3100
 105 CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATCAATTA
 106 CAAGCGGATA CGAATATTGC CATGATTCAT GCGGCAGATA AACGTGTTCA 3200
 107 TAGCATTGCA GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA
 108 ATGCGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTTCAC TGCATTCTCC 3300
 109 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTTTA ATAATGGCTT
 110 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400
 111 AACGTTGCGT CCTTGTGTT CCGBAATGGG AAGCAGAAGT GTCACAAGAA
 112 GTTCGTGTCT GTCCGGGTG TGGCTATATC CTTGCTGTCA CAGCGTACAA 3500
 113 GGAGGGATAT GGAGAAGGT GCGTAACCAT TCATGAGATC GAGAACAATA
 114 CAGACGAAC TGAAGTTTAGC AACTGCGTAG AAGAGGAAAT CTATCCAAAT 3600
 115 AACACGGTAA CGTGAATGA TTATACTGTA AATCAAGAAG AATACGGAGG
 116 TGCCTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAG 3700
 117 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA
 118 GAGAATCCTT GTGAATTTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800
 119 AGTTGSTTAT GTGACAAAAG AATTAGAATA CTTCCAGAA ACCGATAAGG
 120 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTTATCGT GGACAGCGTG 3900
 121 GAATTACTCC TTATGGAGGA A (end HD-73).

49. A process for preparing pesticidal chimeric
 toxin ACB-1 having the following amino acid sequence:

MDN.NPN INECIPYNC LSNFEVEVLGGERIE
 TGYTPIDISLSLTQFL LSEFVFGAGFVLGL
 VDI IWGIFGPSQWDAFLVQIEQLINQRIEE
 FARNQAISRLEGLSNLYQIYAESFREWEAD
 PTNPALREEMRIQFNDMNSALTTAIFLFAV
 QNYQVPLLSVYVQAANLHLSVLRDVS VFGQ
 RWGFDAATINSRYNDLTR LIGNYTDYAVRW
 YN.TGLERVWGPDSRDWVRYNQFRRELT LTV
 LDIVALFPNYDSRRYP IRTVSQLTREIYTN
 PVLENFDGSGFRGSAQGIERSIRSPHLM DIL
 NSITIYTDAHRGY YWSGHQIMASPVGFSG
 PEFTFPLY.GTMGNAAFPQQRIVAQ LGGGVYR

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15  T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
16  G T S S N L P S A V Y R K S G T V D S L N E I P P Q N N N V
17  P P R Q E F S H R L S H V S M F R S G F S N S S V S I I R A
18  P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
19  N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
20  L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
21  I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
22  F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
23  R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
24  S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
25  L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
26  G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
27  T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
28  L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
29  G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
30  L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
31  E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
32  L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
33  Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
34  A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
35  L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
36  N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
37  V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
38  E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
39  N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
40  E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
41  V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
42  E L L L M E E

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43 which comprises culturing a prokaryotic microbe
44 hosting a recombinant DNA transfer vector, denoted
45 pACB-1, comprising DNA having the following nucleotide
46 sequence or equivalent nucleotide sequences containing
47 bases whose translated region codes for the same
48 amino acid sequence:

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49          (start HD-73)          ATG GATAACAATC 400
50  CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
51  GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTACACCC CAATCGATAT 500
52  TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
53  GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
54  CAATGGGACG CATTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT
55  AGAAGAATTC GCTAGGAACC AAGCCATTC TAGATTAGAA GGACTAAGCA 700
56  ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
57  ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
58  CAGTGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
59  TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
60  TTGAGAGATG TTTCAAGTGT TGGACAAAGG TGGGGATTG ATGCCGCGAC

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61 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGSC AACTATACAG 1000
62 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
63 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
64 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
65 ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
66 GTATTAGAAA ATTTTGATGG TAGTTTTCSA GGCTCGGCTC AGGGCATAGA
67 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
68 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA
69 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCT TTCCGCTATA 1400
70 TGGAACTATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
71 GTCAGGGCGT STATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
72 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
73 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
74 GAACGGTAGA TTCGCTGAAT GAAATACCGC CACAGAATAA CAACGTGCCA
75 CCTAGGCAAG AATTTAGTCA TCGATTAGC CATGTTTCAA TGTTTCGTTT 1700
76 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
77 (start HD-1) CCAACGT TTTCTTGSCA GCATCGCAGT 1900
78 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
79 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTGCTT AAAGGACCAG 2000
80 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTTCA
81 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
82 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
83 GAAGACCTAT TAATCAGGGT AATTTTTTCAG CAACTATGAG TAGTGGGAGT 2200
84 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
85 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
86 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
87 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
88 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAACAGAT GTGACGGATT
89 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATTT 2500
90 TGTCTGATG AAAACAAGA ATTGTCCGAG AAGTCAAAC ATGCGAAGCG
91 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACCTTC AGAGGGATCA 2600
92 ATAGACAACCT AGACCGTGSC TGGAGAGGAA GTACGGATAT TACCATCCAA
93 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
94 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
95 TAAAAGCCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
96 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
97 TGTGCCAGGT ACGGGTTCTT TATGSCCGCT TTCAGCCCAA AGTCCAATCG 2900
98 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
99 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000
100 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
101 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
102 CTAGGSAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
103 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
104 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
105 GCTTTATTTG TAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
106 TGCCATGATT CATGCGGCGA ATAAACGTGT TCATAGCATT CGAGAAGCTT
107 ATCTGCTGA GCTGTCTGTG ATTCGSGGTG TCAATGCGGC TATTTTTGAA 3400
108 GAATTAGAAG GBCGTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
109 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
110 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTTGTT
111 CTTCCGGAAT GGGAAAGCAG AGTGTCACAA GAAGTTCGTG TCTGTCCGGG 3600
112 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAA

112 111 110 109 108 107 106 105 104 103 102 101 100 99 98 97 96 95 94 93 92 91 90 89 88 87 86 85 84 83 82 81 80 79 78 77 76 75 74 73 72 71 70 69 68 67 66 65 64 63 62 61

113 GTTGCCTAAC CATTCATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 114 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 115 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 116 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC
 117 TATGAAGAAA AATCGTATAC ASATGGACGA AGAGAGAATC CTTGTGAATT 3900
 118 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 119 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 120 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 121 GGAA (end HD-1) .

1 50. A process for preparing pesticidal chimeric
 2 toxin SYW1 having the following amino acid sequence:

3 MDNNPNIN ECIPYNC LSNPEVE VLGGERIE
 4 TGYTFIDISLSLTQFLLSEFVPGAGFVLGL
 5 VDIIWGIFGFSQWDAFLVQIEQLINQRIEE
 6 FARNQAI SRLEGLSNLYQIYAESFREWEAD
 7 PTNPA LREEMRIQFNDMNSALT TAIP LFAV
 8 QNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
 9 RWGFDAATINSRYNDLTRLIGNYTDYAVRW
 10 YNTGLERVWGPDSRDWVRYNQFRRELTLTV
 11 LDIVALFPNYDSRRYP IRTVSQLTREIYTN
 12 PVLENFDGSGFRGSAQGGIEGSI RSPHLM DIL
 13 NSIT IYTD AHKG EY YWSGHQIMASPVGFSG
 14 PEFTFP LYGT MGN AAPQQRI VAQLGGGVYR
 15 TSSSTLYRRP FNIGINNQQLSVLDGTEFAY
 16 GTSSNLPSAVYRKSGTVDSLDEIPPQNNNV
 17 PPRQGFSHRLSHVSMFRSGFSNS SVSIRA
 18 PTF SWQHRS AEFNNIIPSSQITQIPLTKST
 19 NLGSGT SVVKGP GFTGGDILRRTSPGQIST
 20 LRVNITAPLSQRYRVRIRYASTTNLQFHTS
 21 IDGRPINQGNFSATMSSG SNLQSGSFRTVG
 22 FTT PPNFSNGSSVFTLSAHVFNSGNEVYID
 23 RIEFVPAEVTFEAEYDLERAQKAVNELFTS
 24 SNQIGLKT DVTDYHIDQVSNLVECLSD EFC
 25 LDEKQELSEKVKHAKRLSDERNLLQDPNFR
 26 GINRQLDRGWRGSTDITIQGGDDVFKENYV
 27 TLLGT FDECYPT YLYQKIDESKLKAYTRYQ
 28 LRGYIEDSQDLEIYLIRYN AKHETVNVPGT
 29 GSLWPLSAQSPIGKCGEPNRCAPHLEWNP D
 30 LDCSCR DGEKCAHHS HHFSLDIDVGCTDLN
 31 EDLGVWVIFKIKTQDGHARLGNLEFLEEK P
 32 LVGEALARVKRAEKKWRDKREKLEWETNI V
 33 YKEAKESVDALFVNSQYDQLQADTNIAI H
 34 AADKRVHSIREAYLPELSVIPGVNA AIFEE
 35 LEGRI FTAFSLYDARNV IKN GDFNGLSCW
 36 NVKGHV DVEEQNNQRN SVLVLP EWAEVSE
 37 VRVCPGRGYILRV TAYKEGYGEGCVTIHEI
 38 ENNTDELKFSNCVEEEIYPNNTVTCNDYTV
 39 NQEEYGGAYTSRNRGYN EAPSVPADYASVY
 40 EEKSYTDGRRENPCFNRG YRDYTPLPVGY
 41 VTKELEYFPETDKVWIEIGETEGTFIVDSV
 42 ELL L MEE

43 which comprises culturing a prokaryotic microbe
44 hosting a recombinant DNA transfer vector, denoted
45 pSYW1, comprising DNA having the following nucleotide
46 sequence or equivalent nucleotide sequences containing
47 bases whose translated region codes for the same
48 amino acid sequence:

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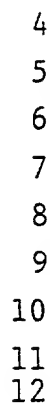
49          (start HD-73)          ATG GATAACAATC 400
50 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
51 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTTACACCC CAATCGATAT 500
52 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
53 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
54 CAATGGGACG CATTCTTGTG ACAAATTGAA CAGTTAATTA ACCAAAGAAT
55 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGAAGTAAAG 700
56 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
57 ACTAATCCAG CATTAGAGAG AGAGATGCGT ATTCAATTCA ATGACATGAA 800
58 CAGTGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
59 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
60 TTGAGAGATG TTTCAGTGTT TGGACAAAGG TGGGGATTTG ATGCCGCGAC
61 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
62 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
63 GATTCTAGAG ATTGGGTAAG GTATAATCAA JTTAGAAGAG AATTAACTACT 1100
64 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
65 ATCCAATTCT AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
66 GTATTAGAAA ATTTTGATGG TAGTTTTCSA GGCTCGGCTC AGGGCATAGA
67 AGGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
68 TCTATACGGA TGCTCATAAA GGGGAATATT ATTGGTCAGG GCATCAAATA
69 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCTT TTCCGCTATA 1400
70 TGGAACTATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
71 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
72 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
73 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
74 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
75 CCTAGGCAAG GATTTAGTCA TCGATTAAAG CATGTTTCAA TGTTTCGTTT 1700
76 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
77          (start HD-1)          CCAACGT TTTCTTGGCA GCATCGCAGT 1900
78 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
79 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
80 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTACCTGCG CCAGATTTCA
81 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
82 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
83 GAAGACCTAT TAATCAGGGT AATTTTTTCA CAACATGAG TAGTGGGAGT 2200
84 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
85 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
86 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
87 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
88 GCTGTTTACT TCTTCCAATC AAATCGGGT AAAAACAGAT GTGACGGATT
89 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTGTTATC AGATGAATTT 2500
90 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
91 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600
92 ATAGACAACG AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA

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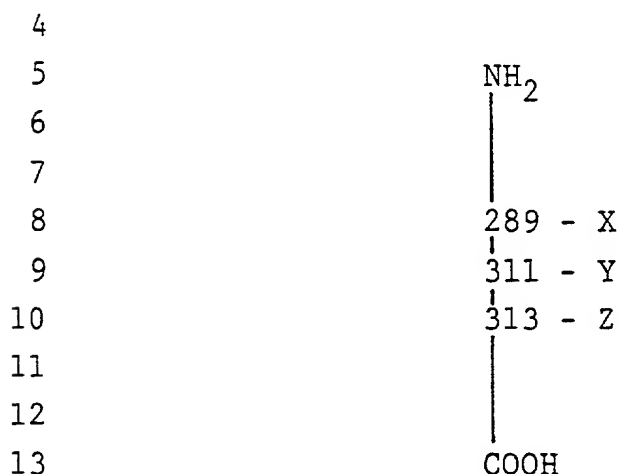
[illegible]

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13 wherein X is one of the 20 common amino acids
14 except Asp when the amino acid at position 425 is
15 Gly; Y is one of the 20 common amino acids except
16 Gly when the amino acid at position 411 is Asp.

1 52. A chimeric toxin, having the amino acid
2 sequence of toxin EW3, with changes which can be shown
3 schematically as follows:



15 wherein X is one of the 20 common amino acids except
16 Arg when the amino acid at position 311 is Arg and the
17 amino acid at position 313 is Tyr; Y is one of the 20
18 common amino acids except Arg when the amino acid at
19 position 289 is Arg and the amino acid at position 313
20 is Tyr; and Z is one of the 20 common amino acids
21 except Tyr when the amino acid at position 289 is
22 Arg and the amino acid at position 311 is Arg.

1 53. DNA encoding a chimeric toxin as shown in
2 claim 51.

1 54. DNA encoding a chimeric toxin as-shown in
2 claim 52.

1 55. A recombinant DNA transfer vector comprising
2 DNA encoding a chimeric toxin as shown in claim 51.

1 56. A recombinant DNA transfer vector comprising
2 DNA encoding a chimeric toxin as shown in claim 52.

1 57. A chimeric toxin comprising the variable
2 region or regions of two or more Bacillus toxins.

1 58. A toxin, according to claim 57, wherein the
2 Bacillus toxins are B. thuringiensis toxins.

1 59. A toxin, according to claim 58, wherein the
2 B. thuringiensis toxins are B. thuringiensis var.
3 kurstaki HD-1 toxin and B. thuringiensis var. kurstaki
4 HD-73 toxin.

1 60. A toxin, according to claim 58, wherein
2 the B. thuringiensis toxins are encoded by a pesticide-
3 producing strain of Bacillus thuringiensis, consisting
4 of B. thuringiensis M-7, B. thuringiensis var. kurstaki,
5 B. thuringiensis var. finitimus, B. thuringiensis var.
6 alesti, B. thuringiensis var. sotto, B. thuringiensis
7 var. dendrolimus, B. thuringiensis var. kenyae, B.
8 thuringiensis var. galleriae, B. thuringiensis var.
9 canadensis, B. thuringiensis var. entomocidus, B.
10 thuringiensis var. subtoxicus, B. thuringiensis var.
11 aizawai, B. thuringiensis var. morrisoni, B. thuringiensis
12 var. ostrinae, B. thuringiensis var. tolworthi, B.
13 thuringiensis var. darmstadiensis, B. thuringiensis
14 var. toumanoffi, B. thuringiensis var. kyushuensis, B.
15 thuringiensis var. thompsoni, B. thuringiensis var.
16 pakistani, B. thuringiensis var. israelensis, B. thurin-
17 giensis var. indiana, B. thuringiensis var. dakota,

18 B. thuringiensis var. tohokuensis, B. thuringiensis
19 var. kumanotoensis, B. thuringiensis var. tochigiensis,
20 B. thuringiensis var. colmeri, B. thuringiensis var.
21 wuhanensis, B. thuringiensis var. tenebrionis, B.
22 thuringiensis var. thuringiensis, and other Bacillus
23 species selected from B. cereus, B. moritai, B.
24 popilliae, B. lentimorbus, and B. sphaericus.